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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:06:05 ; Search time 65.3214 Seconds
(without alignments)
2468.595 Million cell updates/sec

Title: US-09-868-131A-1
Perfect score: 1954
Sequence: 1 MNSSPAGTPSPQPSRANGNI.....ASSAFLGFSVAPEDDILDC 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1954	100.0	367	3 AAY95275	Aay95275 Human ser
2	1954	100.0	367	4 AAU28087	Aau28087 Novel hum
3	1954	100.0	367	5 AAE22765	Aae22765 Human ser
4	1954	100.0	367	7 ADD45799	Add45799 Human pro
5	1954	100.0	367	8 ADI29317	Adi29317 Human MAR
6	1954	100.0	367	8 ADJ45521	Adj45521 LXR-ligan
7	1954	100.0	382	4 AAM25594	Aam25594 Human pro
8	1954	100.0	396	9 ADY37607	Ady37607 Lung canc
9	1954	100.0	427	3 AAY95276	Aay95276 Human ser
10	1954	100.0	427	8 ADQ88284	Adq88284 Human 549
11	1952	99.9	367	4 AAB65708	Aab65708 Novel pro
12	1848	94.6	367	3 AAY95277	Aay95277 Mouse ser
13	1848	94.6	367	7 ADG45797	Adg45797 Rat Prote
14	1767	90.5	398	6 ADA05780	Ada05780 Human NOV
15	1748.5	89.5	398	8 ADN29444	Adn29444 Human NOV
16	1691	86.5	319	4 AAB99838	Aab99838 AGC prote
17	1691	86.5	319	8 ADJ38886	Adj38886 SGK2 amin
18	1677	85.8	335	8 ADP29822	Adp29822 Human sec
19	1665	85.2	330	8 ADN61463	Adn61463 Human Kpp
20	1413	72.3	431	3 AAB24116	Aab24116 Rat serum
21	1413	72.3	431	3 AAY93530	Aay93530 A rat ser
22	1411	72.2	407	7 ADC69794	Adc69794 Human ser
23	1411	72.2	431	2 AAW90139	Aaw90139 Human sgk
24	1411	72.2	431	6 ADA10889	Ada10889 Human cdn

25	1411	72.2	431	7 ADG31708	Adg31708 Human pro
26	1411	72.2	431	7 ADK50982	Adk50982 Human NOV
27	1411	72.2	431	7 ADK50984	Adk50984 Human NOV
28	1411	72.2	431	8 ADO55118	Ado55118 Protein #
29	1411	72.2	431	9 ADY14632	Ady14632 PRO polyp
30	1411	72.2	431	9 ADY19878	Ady19878 PRO polyp
31	1411	72.2	431	9 AEA04529	Aea04529 Human pro
32	1411	72.2	442	7 ADG31706	Adg31706 Human pro
33	1411	72.2	445	7 ADC69792	Adc69792 Human pro
34	1411	72.2	526	6 ADA54293	Ada54293 Human pro
35	1411	72.2	526	7 ADG31710	Adg31710 Human pro
36	1411	72.2	788	7 ADD93289	Add93289 p53-SGK(6
37	1409	72.1	431	8 ADO60030	Ado60030 CRH signa
38	1409	72.1	431	8 ADO44573	Ado44573 Serum/glu
39	1407	72.0	373	4 AAB99815	Aab99815 AGC prote
40	1407	72.0	430	7 ADN95921	Adn95921 Human BEC
41	1407	72.0	431	2 AAW77217	Aaw77217 Human cel
42	1407	72.0	431	3 AAY95279	Aay95279 Human ser
43	1407	72.0	431	3 AAB24115	Aab24115 Human ser
44	1407	72.0	431	4 AAB65613	Aab65613 Novel pro
45	1407	72.0	431	7 ADD14174	Add14174 Human src

ALIGNMENTS

RESULT 1
AAY95275
ID AAY95275 standard; protein; 367 AA.
XX
AC AAY95275;
XX
DT 12-SRP-2000 (first entry)
XX
DE Human serum and glucocorticoid-induced protein kinase 2-alpha.
XX
KW Serum and glucocorticoid-induced protein kinase 2; SGK2-alpha; human;
KW phosphorylation; cancer; diabetes; ischaemia; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 279
FT Modified-site /note= "O-phosphorylated"
FT Modified-site 334
FT Modified-site /note= "O-phosphorylated"
XX
PN WO200035946-A1.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-GB004232.
XX
PR 14-DEC-1998; 98US-0112217P.
PR 19-AUG-1999; 99GB-00019676.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Cohen P, Kobayashi T, Deak M;
XX
DR WPI; 2000-442364/38.
DR N-PSDB; AAA27856.
XX
PT Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)
PT or dephosphorylation, useful for treatment of cancer, diabetes and
XX ischemic diseases.
XX
PS Disclosure; Page 6; 127pp; English.
XX
CC The present sequence is that of human serum and glucocorticoid-induced
CC protein kinase (SGK) isoform 2-alpha. SGK (see AAY95279) was initially
CC identified as a glucocorticoid and osmotic stress-responsive gene. Novel

CC isoforms, SGK2 and SGK3, were isolated from EST database searches, and 2
CC splice variants of SGK2, i.e. SGK2-alpha and -beta (see AY95276), which
CC contains an extra 60 N-terminal residues, were identified. SGK2-alpha is
CC expressed in liver, kidney, pancreas and brain. It is activated by
CC phosphorylation in a similar manner to SGK. The invention provides
CC methods of activating SGK activity by phosphorylation using 3-
CC phosphoinositide-dependent protein kinase-1 (PDK1), and of reducing the
CC activity of SGK by dephosphorylation. The invention also provides a
CC method of identifying a compound that modulates the activity of SGK. Such
CC compounds are useful for treating patients requiring modulation of SGK,
CC such as patients with cancer, diabetes or ischaemic disease
XX
SQ Sequence 367 AA;

Query Match 100.0%; Score 1954; DB 3; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.3e-180;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60
DB 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60
QY 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPPEKLYFVLDYVNGE 120
DB 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPPEKLYFVLDYVNGE 120
QY 121 LFFHLQRRERFLEPRARFYAAEVASIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLEPRARFYAAEVASIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
QY 181 CKEGVEPEDTTFCTGTPSYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPFFVSQDVS 240
DB 181 CKEGVEPEDTTFCTGTPSYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPFFVSQDVS 240
QY 241 QVYENILHPLQIPGRTVAACDLQSLHKQORIGSKADFLKTNHVPFSPINWDDL 300
DB 241 QVYENILHPLQIPGRTVAACDLQSLHKQORIGSKADFLKTNHVPFSPINWDDL 300
QY 301 YHKRLTPFPNPNVTGSPADLKHFDEPTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 360
DB 301 YHKRLTPFPNPNVTGSPADLKHFDEPTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 360
QY 361 DDILDC 367
DB 361 DDILDC 367

RESULT 2
AAU28087
ID AAU28087 standard; protein; 367 AA.

AC AAU28087;

DT 18-DEC-2001 (first entry)

XX Novel human secretory protein, Seq ID No 256.

KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.

XX Homo sapiens.

XX WO200166689-A2.

XX 13-SEP-2001.

XX

PF 05-MAR-2001; 2001WO-US004942.
XX
PR 07-MAR-2000; 2000US-00519705.
PR 19-MAY-2000; 2000US-00574454.
PR 17-JUN-2000; 2000US-00596193.
PR 14-JUL-2000; 2000US-00616847.
PR 19-SEP-2000; 2000US-00665363.
PR 20-OCT-2000; 2000US-00693267.
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX
DR WPI; 2001-589934/66.
DR N-PSDB; AAS44987.
XX
PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis and treatment of
PT cancer, neurological, inflammatory, and autoimmune disorders.
PS Example 4; SEQ ID NO 256; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)
CC and polynucleotides (II). (I) and (II) are useful for treating
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
CC involved in increasing haematopoiesis, stem cell survival, bone growth
CC and remodeling. (I), (II) and modulators of (II) are useful for
CC prophylaxis or treatment of one or more cancers. (II) is also useful for
CC creating transgenic animals useful for studying the in vivo activities of
CC the polypeptide as well as for studying modulators of the polypeptides.
CC (I) induces the proliferation of neural cells and regeneration of nerve
CC and brain tissue and is useful for the treatment of central and
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis and is useful for treating myeloid
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,
CC or periodontal disease. Furthermore, (I) is also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, various immune deficiencies and
CC disorders including severe combined immunodeficiency (SCID), bacterial or
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC reactions and conditions, such as asthma or other respiratory problems.
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
CC fertility, metabolism, catabolism, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU28020-AAU28395 represent novel human secreted protein
CC amino acid sequences of the invention

XX SQ Sequence 367 AA;

Query Match 100.0%; Score 1954; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.3e-180;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60
DB 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60

QY 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPPEKLYFVLDYVNGE 120
DB 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPPEKLYFVLDYVNGE 120
QY 121 LFFHLQRRERFLEPRARFYAAEVASIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180

Db 121 LFFHLQRRERFLEPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTFDGL 180
QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKPEYDRAVDWCLGAVLYEMLHGLPPFYSDVS 240
Db 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKPEYDRAVDWCLGAVLYEMLHGLPPFYSDVS 240
QY 241 QMYENILHQPLOIPGGRTVAACDLQSLHKKDQORLGSKADFLKTNHVFSPINWDDL 300
Db 241 QMYENILHQPLOIPGGRTVAACDLQSLHKKDQORLGSKADFLKTNHVFSPINWDDL 300
QY 301 YHKRLTPPNPNVTGPADLKHFDPFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
Db 301 YHKRLTPPNPNVTGPADLKHFDPFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 361 DDDILDC 367
Db 361 DDDILDC 367

RESULT 3
AAE22765
ID AAE22765 standard; protein; 367 AA.
XX AC AAE22765;
XX DT 09-AUG-2002 (first entry)
XX DE Human serum and glucocorticoid-induced protein kinase, SGK2-alpha.
XX KW Human; cytostatic; antisense gene therapy; screening; protein kinase;
KW cancer; liver; colon; tumour; inflammation; arthritic synovium; enzyme;
KW serum and glucocorticoid-induced protein kinase; SGK2-alpha.
XX OS Homo sapiens.
XX PN WO200224947-A2.
XX PD 28-MAR-2002.
XX PF 20-SEP-2001; 2001WO-1B02237.
XX PR 20-SEP-2000; 2000US-0233999P.
XX PR 02-OCT-2000; 2000US-0237419P.
XX PR 02-OCT-2000; 2000US-0237423P.
XX PR 04-OCT-2000; 2000US-0238558P.
XX PR 10-MAY-2001; 2001US-0290555P.
XX PA (KINE-) KINETEK PHARM INC.
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX Yoganathan T, Delaney AD;
XX WPI; 2002-394145/42.
DR N-PSDB; AAD36141.
XX
PT Diagnosing cancer, comprises determining the upregulation of expression
PT of a nucleic acid sequence encoding a protein kinase or upregulation of
PT expression of the protein kinase, in the cancer.
XX
PS Claim 1; Page 66-67; 87pp; English.
XX
CC The invention relates to a method for screening biologically active agent
CC that modulates cancer associated protein kinase function. The invention
CC also relates to a method for diagnosing cancer comprising determining the
CC upregulation of expression of a nucleic acid sequence encoding a protein
CC kinase. The method is useful for diagnosing cancer. A protein kinase is
CC useful for screening biological agents that modulate cancer associated
CC protein kinase function. Downregulating the activity of protein kinase is
CC useful for inhibiting the growth of a cancer cell, e.g. liver or colon
CC cancer. A nucleic acid encoding protein kinase is useful to screen biopsy
CC derived tumours and inflammatory samples such as arthritic synovium, for
CC amplified DNA in the cell or increased expression of corresponding mRNA
CC or protein and is also useful to detect differences in expression levels

CC such as molecular weight, amino acid and nucleotide sequences between the
CC two cells. The present sequence is human serum and glucocorticoid-induced
CC protein kinase, SGK2-alpha
XX
SQ Sequence 367 AA;

Query Match 100.0%; Score 1954; DB 5; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.3e-180;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPSPSPRANGNINLGPSANPNAQPTDPLFKVIGKNGYKVLAKRKSDGAF 60
Db 1 MNSSPAGTSPSPSPRANGNINLGPSANPNAQPTDPLFKVIGKNGYKVLAKRKSDGAF 60
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120
QY 121 LFFHLQRRERFLEPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTFDGL 180
Db 121 LFFHLQRRERFLEPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTFDGL 180
QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKPEYDRAVDWCLGAVLYEMLHGLPPFYSDVS 240
Db 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKPEYDRAVDWCLGAVLYEMLHGLPPFYSDVS 240
QY 241 QMYENILHQPLOIPGGRTVAACDLQSLHKKDQORLGSKADFLKTNHVFSPINWDDL 300
Db 241 QMYENILHQPLOIPGGRTVAACDLQSLHKKDQORLGSKADFLKTNHVFSPINWDDL 300
QY 301 YHKRLTPPNPNVTGPADLKHFDPFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
Db 301 YHKRLTPPNPNVTGPADLKHFDPFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 361 DDDILDC 367
Db 361 DDDILDC 367

RESULT 4
ADD45799
ID ADD45799 standard; protein; 367 AA.
XX AC ADD45799;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein XP_009494, SEQ ID NO 11468.
XX KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; XP_009494.
XX

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 367 AA;

Query Match 100.0%; Score 1954; DB 7; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.3e-180;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60

QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPPEKLYFVLDYVNGE 120
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPPEKLYFVLDYVNGE 120

QY 121 LFFHLQRRRRFLEPPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db 121 LFFHLQRRRRFLEPPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180

QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPPFYSQDVS 240
Db 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPPFYSQDVS 240

QY 241 QMYENILHQPLOIPGRTVAACDLQLSLHKDQORGLSKADFLFKNHVFFSPINWDDL 300
Db 241 QMYENILHQPLOIPGRTVAACDLQLSLHKDQORGLSKADFLFKNHVFFSPINWDDL 300

QY 301 YHKRLTPPNPNVTGPADLUKHPDFTQBAVSKSIGCTPDTVASSSGASSAFGLFSYAPE 360
Db 301 YHKRLTPPNPNVTGPADLUKHPDFTQBAVSKSIGCTPDTVASSSGASSAFGLFSYAPE 360

QY 361 DDDILDLC 367
Db 361 DDDILDLC 367

RESULT 5
ADI29317
ID ADI29317 standard; protein; 367 AA.
XX
AC ADI29317;

XX 22-APR-2004 (first entry)
DE Human MARK3-associated protein #87.
XX
XX Human; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorder;
KW hyperproliferative disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003232771-A1.
XX
PD 18-DEC-2003.
XX
PF 17-JUN-2002; 2002US-00174319.
XX
PR 17-JUN-2002; 2002US-00174319.
XX (ISIS-) ISIS PHARM INC.
XX Ward DT, Freier SM, Dobie KW;
XX
XX WPI: 2004-052188/05.
DR N-PSDB; ADI29435.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
PT expression of MARK3 or for treating cancer or Alzheimer's disease.
XX
XX Disclosure; SEQ ID NO 237; 233pp; English.
XX
XX The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding MARK3
CC (MAP/microtubule affinity-regulating kinase 3), that specifically
CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression
CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
CC composition comprising the compound and a carrier or diluent, inhibiting
CC the expression of MARK3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with MARK3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer and neurodegenerative diseases e.g.
CC Alzheimer's disease. The present sequence is a MARK3 associated protein
CC included in the figures but not mentioned anywhere else in the
CC specification.
XX SQ Sequence 367 AA;

Query Match 100.0%; Score 1954; DB 8; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.3e-180;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60

QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPPEKLYFVLDYVNGE 120
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPPEKLYFVLDYVNGE 120

QY 121 LFFHLQRRRRFLEPPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db 121 LFFHLQRRRRFLEPPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180

QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPPFYSQDVS 240
Db 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPPFYSQDVS 240

QY 241 QMYENILHQPLOIPGRTVAACDLQLSLHKDQORGLSKADFLFKNHVFFSPINWDDL 300
Db 241 QMYENILHQPLOIPGRTVAACDLQLSLHKDQORGLSKADFLFKNHVFFSPINWDDL 300

XX Identifying a compound for treating a cardiovascular or thrombotic
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
PT and detecting the binding.
XX
PS Claim 1; SEQ ID NO 126; 512pp; English.
PS
XX This invention relates to a novel compound that is capable of treating a
CC cardiovascular or thrombotic disorder. Specifically, it refers to the
CC identification of nucleic acid molecules, and the encoded proteins
CC thereof, which are differentially expressed in cardiovascular disease
CC states relative to their normal expression in non-diseased tissue. The
CC present invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of
CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation,
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,
CC dyslipidaemia, high blood pressure or heart failure. As such, they
CC exhibit cardiant, thrombolytic, anticoagulant, antilipaeamic, hypotensive
CC and cardiant activities. This polypeptide sequence is a human protein
CC that is differentially expressed in a patient with a cardiovascular
CC disorder, given in an exemplification of the invention.
XX
SQ Sequence 427 AA;

Query Match 100.0%; Score 1954; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.5e-180;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRSDGAF 60
Db |||||||
QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRSDGAF 120
Db |||||||
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPKLYFVLDYVNGGE 120
Db |||||||
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPKLYFVLDYVNGGE 180
Db |||||||
QY 121 LFFHLQRRERFLEPPARFYAAEASVAGLYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db |||||||
QY 181 LFFHLQRRERFLEPPARFYAAEASVAGLYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240
Db |||||||
QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVS 240
Db |||||||
QY 241 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVS 300
Db |||||||
QY 241 QMYENILHQPLOIPGGRVVAACDLQSLHKKDQORQLGSKADFLBKHNHFFSPINWDDL 300
Db |||||||
QY 301 QMYENILHQPLOIPGGRVVAACDLQSLHKKDQORQLGSKADFLBKHNHFFSPINWDDL 360
Db |||||||
QY 361 YHKRLTPPNPNVTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
Db |||||||
QY 361 DDILDC 367
Db |||||||
QY 421 DDILDC 427

RESULT 11
AAB65708
ID AAB65708 standard; protein; 367 AA.
XX
AC AAB65708;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase, SEQ ID NO: 237.
XX
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;

KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS Homo sapiens.
XX
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014842.
XX
PR 28-MAY-1999; 99US-0136503P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
DR WPI; 2001-032161/04.
DR N-PSDB; AAF44737.
XX
PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
XX
PS Claim 10; Fig 1; 310pp; English.
XX
CC The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase and
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX
SQ Sequence 367 AA;

Query Match 99.9%; Score 1952; DB 4; Length 367;
Best Local Similarity 99.7%; Pred. No. 2e-180;
Matches 366; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRSDGAF 60
Db |||||||
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPKLYFVLDYVNGGE 120
Db |||||||
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLRYSFQTPKLYFVLDYVNGGE 120
Db |||||||
QY 121 LFFHLQRRERFLEPPARFYAAEASVAGLYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db |||||||
QY 121 LFFHLQRRERFLEPPARFYAAEASVAGLYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db |||||||
QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVS 240
Db |||||||
QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVS 240
Db |||||||
QY 241 QMYENILHQPLOIPGGRVVAACDLQSLHKKDQORQLGSKADFLBKHNHFFSPINWDDL 300
Db |||||||
QY 241 QMYENILHQPLOIPGGRVVAACDLQSLHKKDQORQLGSKADFLBKHNHFFSPINWDDL 300
Db |||||||
QY 301 YHKRLTPPNPNVTGPDALKHFDPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
Db |||||||

Db 301 YHKRLTPFPNVTGPADLKHFDPEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAPE 360
361 DDILDC 367
361 DDILDC 367

RESULT 12
AAV95277
ID AAV95277 standard; protein; 367 AA.
XX AAV95277;
XX 12-SEP-2000 (first entry)
XX Mouse serum and glucocorticoid-induced protein kinase 2.
XX Serun and glucocorticoid-induced protein kinase 2; SGK2; mouse;
KW phosphorylation; cancer; diabetes; ischaemia; therapy.
XX Mus musculus.
XX WO200035946-A1.
XX 22-JUN-2000.
XX 14-DEC-1999; 99WO-GB004232.
XX 14-DEC-1998; 98US-0112217P.
XX 19-AUG-1999; 99GB-00019676.
XX (UYDU-) UNIV DUNDEE.
XX Cohen P, Kobayashi T, Deak M;
XX WPI; 2000-442364/38.
XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)
PT or dephosphorylation, useful for treatment of cancer, diabetes and
PT ischemic diseases.
XX Disclosure; Page 7; 127pp; English.
XX The present sequence is that of mouse serum and glucocorticoid-induced
XX protein kinase (SGK) isoform 2, a protein activated by phosphorylation.
XX The invention provides methods of activating SGK (see also AAV95275-79)
CC by phosphorylation using 3-phosphoinositide-dependent protein kinase-1
CC (PDK1), and of reducing the activity of SGK by dephosphorylation. The
CC invention also provides a method of identifying a compound that modulates
CC the activity of SGK. Such compounds are useful for treating patients
CC requiring modulation of SGK, such as patients with cancer, diabetes or
CC ischaemic disease
XX Sequence 367 AA;
SQ

Query Match 94.6%; Score 1848; DB 3; Length 367;
Best Local Similarity 94.3%; Pred. No. 2.5e-170;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSQDGF 60
Db 1 MASSPVGVPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSQDGF 60

QY 61 YAVKVLQKSLKKKEQSHIMAEVRSVLLKNVRHPLVGLRYSFQTPKLYFLVDYVNGGE 120
Db 61 YAVKVLQKSLKKKEQSHIMAEVRSVLLKNVRHPLVGLRYSFQTPKLYFLVDYVNGGE 120

QY 121 LFFHLQRRERFLEPRARFYTAESAIGYLHSINIIYRDLKPENILLDCQGHVLTDFGL 180
Db 121 LFFHLQRRERFLEPRARFYTAESAIGYLHSINIIYRDLKPENILLDCQGHVLTDFGL 180

QY 181 CKGEVPEPTTSTFCGTPEYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPFPYSQDVS 240
Db 181 CKGEVPEPTTSTFCGTPEYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPFPFNTDVA 240

QY 241 QMYENILHQPLOIPGGRITVAACDLLOSLLHKDQRLGSKADFELEIKNHVFFSPIWDDL 300
Db 241 QMYENILHQPLOIPGGRITVAACDLLOSLLHKDQRLGSKADFELEIKNHVFFSPIWDDL 300

QY 301 YHKRLTPFPNVTGPADLKHFDPEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAPE 360
Db 301 YHKRLTPFPNVTGPADLKHFDPEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAQD 360

QY 361 DDILDC 366
Db 361 DDILDC 366

RESULT 13
ADD45797
ID ADD45797 standard; protein; 367 AA.
XX ADD45797;
XX 29-JAN-2004 (first entry)
XX Rat Protein AAF12756, SEQ ID NO 11466.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; AAF12756.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ

Sequence 367 AA;

Query Match 94.6%; Score 1848; DB 7; Length 367;
Best Local Similarity 94.3%; Pred. No. 2.5e-170;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGSANPNNAQPTDFDLKVIKGNGYKVLAKRKSQDGF 60

Db 1 MASSPVGVSPQPSRANGNINLGSANPNARPTDFDLKVIKGNGYKVLAKRKSQDGF 60

QY 61 YAVKVLQKSIILKKKEQSHIMAEVSALLKNVRHPLVGLRYSFQTPKEKLYFVLDYVNGGE 120

Db 61 YAVKVLQKSIILKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPKEKLYFVLDYVNGGE 120

QY 121 LFFHLQRRERFLEPRARFYAAEVASAIQVLSIIYRDLKPNILLDCQGHVLTDFGL 180

Db 121 LFFHLQRRERFLEPRARFYAAEVASAIQVLSIIYRDLKPNILLDCQGHVLTDFGL 180

QY 181 CKEGVEPEDTTFTFCGTPYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPPFYSDQS 240

Db 181 CKECVEPEETTFTFCGTPYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPPFNTDVA 240

QY 241 QMYENILHQLPIPGRTVAACDLQSLHLKQORQLGSKAFLEIKNHVFPSPINWDDL 300

Db 241 QMYENILHQLPIPGRTVAACDLQSLHLKQORQLGSKDFLDIKNHMFSPINWDDL 300

QY 301 YHKRLTPPNPNVGTGADLKHPDPEFTQEAVSKSIGCTPDTVASSGASSAFLGFSYAPE 360

Db 301 YHKRLTPPNPNVGTGADLKHPDPEFTQEAVSKSIGCTPDTVASSGASSAFLGFSYAQD 360

QY 361 DDDILD 366

Db 361 DDDILD 366

RESULT 14

ADA05780

ID ADA05780 standard; protein; 398 AA.

AC ADA05780;

XX 06-NOV-2003 (first entry)

XX Human NOV33a protein SEQ ID NO:140.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

KW immunomodulator; cytostatic; neurotropic; neuroprotective;

KW antiparkinsonian; antilipemic; gene therapy; human disease;

KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX Homo sapiens.

XX WO2003029424-A2.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327435P.

XX 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329414P.

PR 17-OCT-2001; 2001US-0330142P.

PR 18-OCT-2001; 2001US-0330309P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0339266P.

PR 29-OCT-2001; 2001US-0349575P.

PR 01-NOV-2001; 2001US-0346357P.

PR 17-APR-2002; 2002US-0373260P.

PR 19-APR-2002; 2002US-0373815P.

PR 19-APR-2002; 2002US-0373817P.

PR 19-APR-2002; 2002US-0373884P.

PR 22-APR-2002; 2002US-0374977P.

PR 16-MAY-2002; 2002US-0381037P.

PR 16-MAY-2002; 2002US-0381038P.

PR 17-MAY-2002; 2002US-0381042P.

PR 28-MAY-2002; 2002US-0383656P.

PR 29-MAY-2002; 2002US-0383831P.

PR 25-JUN-2002; 2002US-0391335P.

PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

XX Patturajan M, Sytek KA, Edinger SR, Ellerman K, Malyankar UM;

XX Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;

XX Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;

XX Shinkels RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

XX Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

XX N-PSDB; ADA05779.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing,

XX preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,

XX cancer or dyslipidemia, and in chromosome mapping, tissue typing or

XX pharmacogenomics.

XX Claim 1; Page 219; 586pp; English.

XX The present invention describes NOVX proteins, where X can be 1 to 55

XX (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

XX described above and a carrier; (2) a kit comprising, in one or more

XX containers, the composition described above; (3) an isolated nucleic acid

XX molecule which encodes a NOVX protein of the invention; (4) a vector

XX comprising the nucleic acid molecule described above; (5) a cell

XX comprising the above vector; (6) an antibody that immunospecifically

XX binds to the polypeptide described above; (7) methods for determining the

XX presence or amount of the above polypeptide or nucleic acid molecule in a

XX sample; (8) methods for determining the presence of or predisposition to

XX a disease associated with altered levels of expression of the above

XX polypeptide or nucleic acid molecule in a first mammalian subject; (9) a

XX method of identifying an agent that binds to the polypeptide described

XX above; (10) a method for identifying a potential therapeutic agent for

XX use in treating a pathology that is related to an aberrant expression or

XX aberrant physiological interactions of the polypeptide; (11) a method of

XX screening for a modulator of activity or of latency or predisposition to

XX a pathology associated with the polypeptide; (12) a method for modulating

XX the activity of the polypeptide described above; (13) methods of treating

XX or preventing a pathology associated with the above polypeptide in a

XX mammal; and (14) a method for producing the above polypeptide. NOVX

XX sequences have antidiabetic, anorectic, antibacterial, virucide,

XX immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian

XX and antilipemic activities, and can be used in gene therapy. The

XX polypeptide is useful in manufacturing a medicament for treating a

XX syndrome associated with a human disease. The polypeptide or the nucleic

CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
XX present invention.

XX Sequence 398 AA;

Query Match 90.5%; Score 1767.5; DB 6; Length 398;
Best Local Similarity 92.1%; Pred. No. 1.8e-162;
Matches 338; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 60
DB 61 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 120
QY 61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHFFLVGLRYSFQTPEKLYFVLDYVNGGE 120
DB 121 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHFFLVGLRYSFQTPEKLYFVLDYVNGGE 180
QY 121 LFFHLQRRERFLEPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
DB 181 LFFHLQRRERFLEPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQ----- 230
QY 181 CKGEVPEPTSTFCGTPEVLAPEVLKSPYDAVDWVCGVLYEMLHGLPFPYSODYS 240
DB 231 -----YLAPEVLKSPYDAVDWVCGVLYEMLHGLPFPYSQDVS 271
QY 241 QMVENILHQLPIPGGRTVAACDLQLLHKQORQLGSKADFLKKNHFFSPINWDDL 300
DB 272 QMVENILHQLPIPGGRTVAACDLQLLHKQORQLGSKADFLKKNHFFSPINWDDL 331
QY 301 YHKRLTPPNVNTGPDALKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 360
DB 332 YHKRLTPPNVNTGPDALKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 391
QY 361 DDDILDC 367
DB 392 DDDILDC 398

RESULT 15

ADN62944

ID ADN62944 standard; protein; 398 AA.

XX AC

XX ADN62944;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV33a.

XX OS human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;

KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;

KW wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

XX XX

XX 26-FEB-2004.

XX XX

XX 01-OCT-2002; 2002US-00262511.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327435P.

XX 09-OCT-2001; 2001US-0327449P.

XX 09-OCT-2001; 2001US-0327917P.

XX 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.

XX (SMIT/) SMITHSON G.

PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.

PA (KEKU/) KERUDA R.

PA (JUJU/) JU J.

PA (LILL/) LI L.

PA (GUOX/) GUO X.

PA (PATT/) PATTURAJAN M.

PA (SPYT/) SPYTEK K A.

PA (EDIN/) EDINGER S R.

PA (ELLE/) ELLERMAN K.

PA (MALY/) MALYANKAR U M.

PA (ORTT/) ORT T.

PA (GORM/) GORMAN L.

PA (ZERH/) ZERHUSEN B D.

PA (ANDE/) ANDERSON D W.

PA (ZHON/) ZHONG M.

PA (CATT/) CATTERTON E.

PA (JIWW/) JI W.

PA (MILL/) MILLER C E.

PA (RAST/) RASTELLI L.

PA (STON/) STONE D J.

PA (PENNA/) PENNA C E A.

PA (SHEN/) SHENOY S G.

PA (SHIM/) SHIMKETS R A.

PA (ROTH/) ROTHENBERG M E.

PA (LEAC/) LEACH M D.

PA (AGBE/) AGEE M L.

PA (BERG/) BERGHS C.

PA (DIPI/) DIPPO V A.

PA (EISE/) EISEN A.

PA (GANG/) GANGOLLI E A.

PA (RIEG/) RIEGER D K.

PA (SPAD/) SPADERNA S K.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;

PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno SG;

PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI: 2004-213931/20.

XX N-PSDB; ADN62943.

DR

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,

PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

XX

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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:21:11 ; Search time 17.3113 Seconds
(without alignments)
1752.724 Million cell updates/sec

Title: US-09-868-131A-1
Perfect score: 1954
Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFLGFSYAPEDDDILDC 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1411	72.2	407	2	US-10-067-977-4
2	1411	72.2	445	2	US-10-067-977-2
3	1407	72.0	431	2	US-09-031-295-2
4	1407	72.0	431	2	US-10-000-039-2
5	1404.5	71.9	430	1	US-08-712-709-9
6	1404.5	71.9	430	2	US-09-111-444-9
7	1404.5	71.9	430	2	US-09-541-228-9
8	1403	71.8	431	1	US-08-712-709-5
9	1403	71.8	431	2	US-09-111-444-5
10	1403	71.8	431	2	US-09-541-228-5
11	886	45.3	479	2	US-09-771-161A-246
12	886	45.3	479	2	US-09-771-161A-247
13	886	45.3	479	2	US-09-771-161A-248
14	878.5	45.0	465	2	US-09-526-043-2
15	878.5	45.0	480	2	US-09-590-740-6
16	877.5	44.9	454	2	US-09-526-043-17
17	876	44.8	480	2	US-09-526-043-13
18	876	44.8	481	2	US-09-538-092-1054
19	874.5	44.8	480	2	US-09-091-058-2
20	874.5	44.8	480	2	US-09-590-740-2
21	874.5	44.8	480	2	US-09-538-092-1053
22	874.5	44.8	480	2	US-09-526-043-14
23	874.5	44.8	480	2	US-09-771-161A-223
24	874.5	44.8	726	2	US-09-417-197-71
25	874.5	44.8	727	2	US-09-417-197-139
26	856	43.8	417	2	US-09-590-740-4
27	849.5	43.5	480	2	US-09-205-658-157

28	844.5	43.2	470	2	US-09-248-796A-18482	Sequence 18482, A
29	791	40.5	587	1	US-08-313-274-2	Sequence 2, Appli
30	791	40.5	655	2	US-09-949-016-11676	Sequence 11676, A
31	789.5	40.4	637	2	US-09-817-310-2	Sequence 2, Appli
32	789.5	40.4	637	2	US-10-355-724A-2	Sequence 2, Appli
33	788.5	40.4	482	2	US-09-430-564-2	Sequence 2, Appli
34	788.5	40.4	495	2	US-09-430-564-3	Sequence 3, Appli
35	788.5	40.4	495	2	US-09-762-258-2	Sequence 2, Appli
36	788	40.3	546	2	US-09-205-658-155	Sequence 155, App
37	783.5	40.1	541	2	US-09-205-658-154	Sequence 154, App
38	778	39.8	502	2	US-09-538-092-996	Sequence 996, App
39	778	39.8	525	1	US-08-749-902-7	Sequence 7, Appli
40	778	39.8	525	1	US-08-749-902-8	Sequence 8, Appli
41	778	39.8	525	2	US-09-430-564-16	Sequence 16, Appli
42	778	39.8	525	2	US-09-762-258-4	Sequence 4, Appli
43	769	39.4	568	2	US-09-949-016-7970	Sequence 7970, Ap
44	769	39.4	584	2	US-09-842-307-2	Sequence 2, Appli
45	765	39.2	737	2	US-09-772-647-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-067-977-4
; Sequence 4, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-4

Query Match		72.2%;	Score 1411;	DB 2;	Length 407;
Best Local Similarity		71.2%;	Pred. No. 2.2e-131;		
Matches 262;		Conservative 53;	Mismatches 45;	Indels 8;	Gaps 3;
QY	1	MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDGAF	60		
Db	45	MNANP--SPPSPSQ---QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVF	99		
QY	61	YAVKVLQKKSILKKKEQSHMAERSVLLKNVHPFLVGLRYSPOTPEKLYFVLVYNGGE	120		
Db	100	YAVKVLQKKAIIKKKEKHIMSERNVLLKNVHFLVGLHFSQFADKLYFVLVYINGGE	159		
QY	121	LFPHLQRRERFLPRARFYAAEVAISAIGYLHSLNIYRDLKPENILLCCQGHVLTDFGL	180		
Db	160	LFYHLQRECFLEPRARFYAAEIASALGYLHSLNIYRDLKPENILLDSQGHVLTDFGL	219		
QY	181	CKGEVEPDYTTTFCGTPEYLAPEVLKPEYDRAVDMWCLGAVLYBMLHGLPPFYSDQS	240		
Db	220	CKENIEHNSVTTTFCGTPEYLAPEVLKPEYDRTDWMCLGAVLYBMLYGLPPFYSRNTA	279		
QY	241	QMYENILHQPLOIPGRTVAACDILLQSLHKDQRLSKADFLKKNHVFSPINWDDL	300		
Db	280	EMYDNLNKLPLKPNITNSARHLLEGQLQKDKTRKLGAKDDFMETKSHVFFSLINWDDL	339		
QY	301	YHKRLTPPNPNVTGPADLKHFDPDPEFTQEA VSKSIGCTPDTV---ASSGASSAFGLFSY	357		
Db	340	INKKITPPNPNVSGPNDLRHFDPEFTPEVPVNSIGKSPDSVLVTASVKEAAEALGFSY	399		
QY	358	AFEDDDIL 365			

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Db 400 APPTDSFL 407

RESULT 2
US-10-067-977-2
; Sequence 2, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-2

Query Match 72.2%; Score 1411; DB 2; Length 445;
Best Local Similarity 71.2%; Pred. No. 2.5e-131;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

QY 1 MNS$PAGTSP$OP$RANGNINL$GPSANPN$AQTDF$KLVIGKNGY$KVL$AKR$KSDGAF 60
Db 83 MNANP--$PP$PSQ--QINL$GPSN$PHAK$PSDF$H$KLVIGK$SGF$KVL$ARH$KAEV$F 137
QY 61 YAVKVLQK$K$IL$KKEQ$H$MAERSV$LLKNV$R$P$F$LVGL$RYS$F$Q$T$P$E$K$LY$F$V$L$D$Y$N$G$G$E 120
Db 138 YAVKVLQK$K$IL$KKEQ$H$MAERSV$LLKNV$R$P$F$LVGL$RYS$F$Q$T$P$E$K$LY$F$V$L$D$Y$N$G$G$E 197
QY 121 L$F$H$Q$R$R$F$LE$P$R$A$R$F$Y$A$E$V$A$S$A$IG$Y$L$H$S$N$II$Y$R$D$K$P$EN$ILL$D$C$Q$H$V$LT$D$F$G$L 180
Db 198 L$F$H$Q$R$C$F$LE$P$R$A$R$F$Y$A$E$V$A$S$A$IG$Y$L$H$S$N$II$Y$R$D$K$P$EN$ILL$D$C$Q$H$V$LT$D$F$G$L 257
QY 181 C$K$E$G$E$P$E$D$T$T$F$C$G$T$P$E$Y$L$A$P$E$V$L$R$K$E$P$Y$D$R$A$V$D$M$W$C$L$G$A$V$L$E$M$L$H$G$L$P$P$Y$S$Q$D$V$S 240
Db 258 C$K$E$N$E$H$N$T$T$T$F$C$G$T$P$E$Y$L$A$P$E$V$L$H$K$Q$P$Y$D$R$T$D$M$W$C$L$G$A$V$L$E$M$L$H$G$L$P$P$Y$S$R$N$T$A 317
QY 241 Q$M$Y$N$IL$H$Q$P$IQ$P$G$R$T$V$A$C$D$LL$Q$S$LL$H$K$Q$R$Q$R$G$S$K$A$D$F$E$IK$N$H$V$F$F$S$P$IN$W$D$D$L 300
Db 318 E$M$Y$D$N$IL$N$K$P$L$Q$K$P$N$IT$N$S$A$R$H$L$E$G$L$J$Q$K$D$R$T$K$R$L$G$A$K$D$D$F$M$E$IK$H$V$F$F$S$L$IN$W$D$D$L 377
QY 301 Y$H$K$R$L$T$P$P$N$V$N$T$G$P$A$D$L$K$H$F$D$P$E$T$Q$B$A$V$S$K$S$IG$C$T$P$D$T$V$---A$S$S$G$A$S$A$F$L$G$F$S$Y 357
Db 378 I$N$K$K$IT$P$P$N$V$N$G$P$N$D$L$R$H$F$D$P$E$T$E$P$V$P$N$S$IG$K$S$P$D$S$V$L$V$T$A$S$V$K$E$A$E$A$F$L$G$F$S$Y 437
QY 358 A$P$E$D$D$D$IL 365
Db 438 A$P$T$D$S$F$L 445

RESULT 3
US-09-031-295-2
; Sequence 2, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-031-295-2

Query Match 72.0%; Score 1407; DB 2; Length 431;
Best Local Similarity 70.9%; Pred. No. 5.8e-131;
Matches 261; Conservative 54; Mismatches 45; Indels 8; Gaps 3;

QY 1 MNS$PAGTSP$OP$RANGNINL$GPSANPN$AQTDF$KLVIGKNGY$KVL$AKR$KSDGAF 60
Db 69 MNANP--$PP$PSQ--QINL$GPSN$PHAK$PSDF$H$KLVIGK$SGF$KVL$ARH$KAEV$F 123
QY 61 YAVKVLQK$K$IL$KKEQ$H$MAERSV$LLKNV$R$P$F$LVGL$RYS$F$Q$T$P$E$K$LY$F$V$L$D$Y$N$G$G$E 120
Db 124 YAVKVLQK$K$IL$KKEQ$H$MAERSV$LLKNV$R$P$F$LVGL$RYS$F$Q$T$P$E$K$LY$F$V$L$D$Y$N$G$G$E 183
QY 121 L$F$H$Q$R$R$F$LE$P$R$A$R$F$Y$A$E$V$A$S$A$IG$Y$L$H$S$N$II$Y$R$D$K$P$EN$ILL$D$C$Q$H$V$LT$D$F$G$L 180
Db 184 L$F$Y$H$Q$R$C$F$LE$P$R$A$R$F$Y$A$E$V$A$S$A$IG$Y$L$H$S$N$II$Y$R$D$K$P$EN$ILL$D$C$Q$H$V$LT$D$F$G$L 243
QY 181 C$K$E$G$E$P$E$D$T$T$F$C$G$T$P$E$Y$L$A$P$E$V$L$R$K$E$P$Y$D$R$A$V$D$M$W$C$L$G$A$V$L$E$M$L$H$G$L$P$P$Y$S$Q$D$V$S 240
Db 244 C$K$E$N$E$H$N$T$T$T$F$C$G$T$P$E$Y$L$A$P$E$V$L$H$K$Q$P$Y$D$R$T$D$M$W$C$L$G$A$V$L$E$M$L$H$G$L$P$P$Y$S$R$N$T$A 303
QY 241 Q$M$Y$N$IL$H$Q$P$IQ$P$G$R$T$V$A$C$D$LL$Q$S$LL$H$K$Q$R$Q$R$G$S$K$A$D$F$E$IK$N$H$V$F$F$S$P$IN$W$D$D$L 300
Db 304 E$M$Y$D$N$IL$N$K$P$L$Q$K$P$N$IT$N$S$A$R$H$L$E$G$L$J$Q$K$D$R$T$K$R$L$G$A$K$D$D$F$M$E$IK$H$V$F$F$S$L$IN$W$D$D$L 363
QY 301 Y$H$K$R$L$T$P$P$N$V$N$T$G$P$A$D$L$K$H$F$D$P$E$T$Q$B$A$V$S$K$S$IG$C$T$P$D$T$V$---A$S$S$G$A$S$A$F$L$G$F$S$Y 357
Db 364 I$N$K$K$IT$P$P$N$V$N$G$P$N$D$L$R$H$F$D$P$E$T$E$P$V$P$N$S$IG$K$S$P$D$S$V$L$V$T$A$S$V$K$E$A$E$A$F$L$G$F$S$Y 423
QY 358 A$P$E$D$D$D$IL 365
Db 424 A$P$T$D$S$F$L 431

RESULT 4
US-10-000-039-2
; Sequence 2, Application US/10000039
; Patent No. 6855520
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
```

COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/000,039
FILING DATE: 04-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/031,295
FILING DATE: 26-FEB-1998
APPLICATION NUMBER: DE 197-08-173.8
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 058315/0123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-000-039-2

Query Match 72.0%; Score 1407; DB 2; Length 431;
Best Local Similarity 70.9%; Pred. No. 5.8e-131;
Matches 261; Conservative 54; Mismatches 45; Indels 8; Gaps 3;
QY 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNKGVLLAKRKSDGAF 60
DB 69 MNANP--SPPPSPQ--QINLGPSSNPHAKPSDFHFLKVIKGVSGFKVLLARHKAEEVF 123
QY 61 YAVKVLQKSIILKKKEQSHIMARSVLLKNVRHPLVGLRYSFQTPKLYFVLDYNGGE 120
DB 124 YAVKVLQKAILKKKEKHIMSRNVLKNVHPFLVGLHFSFQTADKLYFVLDYNGGE 183
QY 121 LFFHLQRRERFLEPRARFYAAEVAASAGVLSHLSNIIYRDLKPNILLDCQGHVLTDFGL 180
DB 184 LFFHLQRRERFLEPRARFYAAEIASAGVLSHLSNIIYRDLKPNILLDSQGHVLTDFGL 243
QY 181 CKEGVEPEDTTSTFCCTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240
DB 244 CKENIEHNSTTSTFCCTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 303
QY 241 QMYENILHQLPIPGGRTVAACDLQSLHKKQORLGSKADFLKKNHVFSPINWDDL 300
DB 304 EMYDNLINKPLQKPNITNSARHLLEGLLQKORTKLGAKDDFMETKSHVFFSLINWDDL 363
QY 301 YHKRLTPPNPNVTGPADLKHPDPEFTQEAIVSKSIGCTPDVT---ASSGSASSAFGLFSY 357
DB 364 INKKTTPPNPNVSGPNELRHPDPEFTPEPVPNSIGKSPDSVLVLTASVKEAAEAFGLFSY 423
QY 358 APEDDDIL 365
DB 424 APPTDSFL 431

RESULT 5
US-08-712-709-9
; Sequence 9, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-08-712-709-9

Query Match 71.9%; Score 1404.5; DB 1; Length 430;
Best Local Similarity 70.9%; Pred. No. 1e-130;
Matches 261; Conservative 56; Mismatches 42; Indels 9; Gaps 4;
QY 1 MNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVIKGNKGVLLAKRKSDGAF 60
DB 69 MNANP--SPPPSPQ--QINLGPSSNPHAKPSDFHFLKVIKGVSGFKVLLARHKAEEAF 123
QY 61 YAVKVLQKSIILKKKEQSHIMARSVLLKNVRHPLVGLRYSFQTPKLYFVLDYNGGE 120
DB 124 YAVKVLQKAILKKKEKHIMSRNVLKNVHPFLVGLHFSFQTADKLYFVLDYNGGE 183
QY 121 LFFHLQRRERFLEPRARFYAAEVAASAGVLSHLSNIIYRDLKPNILLDCQGHVLTDFGL 180
DB 184 LFFHLQRRERFLEPRARFYAAEIASAGVLSHLSNIIYRDLKPNILLDSQGHVLTDFGL 243
QY 181 CKEGVEPEDTTSTFCCTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 240
DB 244 CKENIEHNSTTSTFCCTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSDQVS 303
QY 241 QMYENILHQLPIPGGRTVAACDLQSLHKKQORLGSKADFLKKNHVFSPINWDDL 300
DB 304 EMYDNLINKPLQK--NITNSARHLLEGLLQKORTKLGAKDDFMETKSHVFFSLINWDDL 362
QY 301 YHKRLTPPNPNVTGPADLKHPDPEFTQEAIVSKSIGCTPDVT---ASSGSASSAFGLFSY 357
DB 363 INKKTTPPNPNVSGPDLRHPDPEFTPEPVPSSIGRSPDSILVLTASVKEAAEAFGLFSY 422
QY 358 APEDDDIL 365
DB 423 APPMDSFL 430

RESULT 6
US-09-111-444-9
; Sequence 9, Application US/09111444
; Patent No. 6045792

GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-09-111-444-9

Query Match 71.9%; Score 1404.5; DB 2; Length 430;
Best Local Similarity 70.9%; Pred. No. 1e-130;
Matches 261; Conservative 56; Mismatches 42; Indels 9; Gaps 4;
QY 1 MNSSPAGTSPQSPSRANGNINLGPANPNAPQPTDFDLKVIKGNKGVKLLAKRKSDGAF 60
DB 69 MNANP--SPPPSPSQ---QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEAF 123
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120
DB 124 YAVKVLQKKAALKKKEKHIMSERVLLKNVKHPLVGLHFSFQADKLYFVLDYINGE 183
QY 121 LFFHLQRRRFLPEPRARFYAAEVAASAIYGLHSLNIYRDLPENILLDCQGHVLTDFGL 180
DB 184 LFFHLQRRERCFLEPRARFYAAEIASALGYLHSLNIYRDLPENILLDSQGHVLTDFGL 243
QY 181 CKGEVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMHLGLPPFYSDVVS 240
DB 244 CKENIEHNGTTSTFCGTPEYLAPEVLKRPYDRTVDWCLGAVLYEMHLGLPPFYSRNTA 303
QY 241 QMYENILHQPQIPGGRTVAAACDLQLSLHDKQORLQSKADFLKHNHVFSPINWDDL 300
DB 304 EMYDNLNKPQLK-NITNSARHLLGLELLQKDRTKRLGAKDDFMEIKSHIFFSLINWDDL 362
QY 301 YKRLITPPNPVNTGPAADLKHPDPTQBAVSKSGCTPTDV---ASSGASSAFLGFSY 357
DB 363 INKKTTPPNPNVSGPSDLRHFDPTEFPVPSIGRSPDSILVTASVKEAAEAFLGFSY 422
QY 358 APEDDDIL 365

Db 423 APPMDSFL 430
RESULT 7
US-09-541-228-9
Sequence 9, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-09-541-228-9
Query Match 71.9%; Score 1404.5; DB 2; Length 430;
Best Local Similarity 70.9%; Pred. No. 1e-130;
Matches 261; Conservative 56; Mismatches 42; Indels 9; Gaps 4;
QY 1 MNSSPAGTSPQSPSRANGNINLGPANPNAPQPTDFDLKVIKGNKGVKLLAKRKSDGAF 60
DB 69 MNANP--SPPPSPSQ---QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEAF 123
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120
DB 124 YAVKVLQKKAALKKKEKHIMSERVLLKNVKHPLVGLHFSFQADKLYFVLDYINGE 183
QY 121 LFFHLQRRRFLPEPRARFYAAEVAASAIYGLHSLNIYRDLPENILLDCQGHVLTDFGL 180
DB 184 LFFHLQRRERCFLEPRARFYAAEIASALGYLHSLNIYRDLPENILLDSQGHVLTDFGL 243
QY 181 CKGEVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWCLGAVLYEMHLGLPPFYSDVVS 240
DB 244 CKENIEHNGTTSTFCGTPEYLAPEVLKRPYDRTVDWCLGAVLYEMHLGLPPFYSRNTA 303
QY 241 QMYENILHQPQIPGGRTVAAACDLQLSLHDKQORLQSKADFLKHNHVFSPINWDDL 300
DB 304 EMYDNLNKPQLK-NITNSARHLLGLELLQKDRTKRLGAKDDFMEIKSHIFFSLINWDDL 362

Qy	301	YHKRIPTFPNNVTCPADLKHDPDEFTEQAEVSKIGCTPDTV---ASSSGASSAFILGFSY	357
		: : : : : : : : : : : : : : :	
Db	363	INKTKITPFNNVNSGPSDLRHFDEFTTEEPVFPSIGRSDDLSILVTASVKAAEAFLGFSY	422
		: : : : : : : : : : : : : : :	
Qy	358	APEDDDIIL	365
Db	423	APPMDSFL	430

RESULT 8

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US-08-712-709-5
; Sequence 5, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Guegler, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,709
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-08-712-709-5

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Query Match	71.8%;	Score 1403;	DB 1;	Length 431;
Best Local Similarity	70.9%;	Pred. No. 1.5e-130;		
Matches 261;	Conservative 53;	Mismatches 46;	Indels 8;	Gaps 3
Qy	1	MNSSPAGTPSPQPSRANGNINLGPSANPNAPQTFD	FKLVIGKNGYGVLLAKR	SDGAF 60
Db	69	MNANP--SPPSPSQ---QINLGPSSPHAKPSDFH	FLKLVIGKSGFGKVLARHKAEEVF	123
Qy	61	YAVKVLQKGSILKKKGKOSHMAERSVLLKNVRH	PFLVGLRYSPQTPEKLYFVL	DYVNGGE 120
Db	124	YAVKVLQKAILKKKEBKHMISERNVLLKNVGP	PFLVGLHFSQPTADKLYFVL	DYINGGE 183
Qy	121	LFPHLQRRRRLEPRAPFYAAEASATGYLHSLNI	IYRDLKPNILLDCQGHVLT	DFGL 180
Db	184	LFYHLQRECFLEPRAPSYAAEIASALGYLHSLN	IYTRDLKPNILLDSQGHVLT	DFGL 243
Qy	181	CKEGVEPEDTTSTFCGTPYLAPEVLARKPEYD	RAVDWMCIGAVLYEMLHGLPPF	SQDVS 240
Db	244	CKENIEHNSTTSTFCGTPYLAPEVLHKKQPYD	RTVDWMCIGAVLYEMLGGLPPF	SRNTA 303

Qy	241	QMVENILHQPIQIEGGRVAA	CDLLQSLHHKQDQRLGSKADFLRIKXHVFFSPINWDDL	300
Db	304	EMYDNLINKPLOLQPNITNS	SARHLEGLLQKDTKELGAKODFMEIKSHVFFSLINWDDL	363
Qy	301	YHKRLTTPFPNPNTGPADL	KHDFEFTQEAUVSKSGCTPDTV---	ASSGASAFILGFSY 357
Db	364	INKKITPPFPNPVSGPNDL	RHDFEFTPEEPVNSIGKSPDSVLVTASVKAEAEFLGFSY	423
Qy	358	APEDDDIL	365	
Db	424	APPTDSEL	431	

RESULT 9

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US-09-111-444-5
; Sequence 5, Application US/09111444
; Patent No. 6045792
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,444
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-09-111-444-5

```

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Query Match      71.8%; Score 1403; DB 2; Length 431;
Best Local Similarity 70.9%; Pred. No. 1.5e-130;
Matches 261; Conservative 53; Mismatches 46; Indels 8; Gaps 3;
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Qy	121	LPFHLOQRERFLPEPRARFVAABEASAIQYLHSLNIIYRDLKPNENILLDCOCHGVVLTFDGL	180
Db	184	LPFHLQQRFCFLPEPRARSAAEIASALGYLHSLNIVYRDLKPNENILLDSQGHITVLTFDGL	243
Qy	181	CKEGVEPEDTSTFGCTPEYLAPELVRKEPVDRAVDMWCLGAVLYEMLHGLPPFYSDQVS	240
Db	244	CKENIEHNSTSTFGCTPEYLAPELVHLHKQPYDRVDMWCLGAVLYEMLYGLPFPYSBNTA	303
Qy	241	QWYENILHQPLOIQPGRTVAAQCDLLQSLLLHKDQQRQLGSKADFLEIKHNVFFSPINWDDL	300
Db	304	EMYDNLINLKPLQKPNITNSARHLLLEGULLQDRTKRLGAKDDFMEIKSHVFFSLINWDDL	363
Qy	301	YHKRLTTPPNPNVNTGPADLKHDFDEPFTOEAVYSKISGCTPDTV--ASSSCGSAFAGFSY	357
Db	364	INKKITYPPPNPNVNSGPNLDRHDFDEPFTPEEPVNSIGKSPDVLVTASVKAEAAEAFGLFSY	423
Qy	358	APEDDDIL	365
Db	424	APPTDSFL	431

```

RESULT 10
US-09-541-228-5
; Sequence 5, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541.228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712.709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-09-541-228-5

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Db	69	MNANP--SPPPSPQ---QINLGPSSNPHAKSPDFHLKVYIGKSGFKVLLARHKAEEVF	123
Qy	61	YAVKVLQKSKLKKEQSHMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLVDYVNGGE	120
Db	124	YAVKVLQKAILKKKEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLVDYNGGE	183
Qy	121	LFPHLQRRERFLPRARFYAAEVASAIYGLHLSLNIYYRDLKPENILLDCQGHVLTDFGL	180
Db	184	LFVHLQRECFLEPRARSYAAETASALGYLHLSLNIYYRDLKPENILLDSQGHVLTDFGL	243
Qy	181	CKEGVPEPDTTSTFCCTPEYLAPBEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYQDVVS	240
Db	244	CKENIEHNSTTSTFCCTPEYLAPBEVLHQPYDRTDVDMWCLGAVLYEMLYGLPPFYSRNTA	303
Qy	241	QMYENILHOPLOQIPGGRTVAACDLLQSLHKDQORLGSKADFLEIKNVHFFSPINWDDL	300
Db	304	EMVDNILNKPLOKLQPNITNSARHLLGLQKRTKGLGAKDDPWEIKSHVFFSLIINWDDL	363
Qy	301	YHKRLTPPPNPVNTVGPADLKHDFDEPETOBAVSKSIGCTPDTV---ASSSGASSAFLGFSY	357
Db	364	INKKITPPPNPNVSGPNDLRHDFDEPTEPVPNPSICKSPDSVLVTASVKEAEEAFLGFSY	423
Qy	358	APEDDDIL 365	
Db	424	APPTDSFL 431	
RESULT 11			
US-09-771-161A-246			
; Sequence 246, Application US/09771161A			
; Patent No. 6936450			
; GENERAL INFORMATION:			
; APPLICANT: LEVINE, et al.			
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES			
; FILE REFERENCE: 802620-2005.1			
; CURRENT APPLICATION NUMBER: US/09/771,161A			
; CURRENT FILING DATE: 2001-01-26			
; PRIOR APPLICATION NUMBER: 09/724,676			
; PRIOR FILING DATE: 2000-11-28			
; PRIOR APPLICATION NUMBER: 136776			
; PRIOR FILING DATE: 2000-06-15			
; PRIOR APPLICATION NUMBER: 135619			
; PRIOR FILING DATE: 2000-04-12			
; NUMBER OF SEQ ID NOS: 273			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 246			
; LENGTH: 479			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-771-161A-246			

Query Match	45.3%	Score 886;	DB 2;	Length 479;
Best Local Similarity	48.4%;	Pred. No. 3.5e-79;		
Matches 181;	Conservative 55;	Mismatches 100;	Indels 38;	Gaps 8;
Qy	1	MNSSPAGTSPQPSRAN--GNINLGPSANPNAOPT--DFDFLKVIKGNVGVKLLAKRKS	56	
Db	117	MNCSPT-----SQIDNIGEEMDASTTHHKEKTWDFYLLKLGKGTFGKVLVREKA	169	
Qy	57	DGAFYAVKVLQKSLIKKKEQSHIMAEKSVLLKNVRHPFLGVLGRYFQTPKLYFVLDYV	116	
Db	170	SGKYAYMKILKKEVIAKDEVAHTLTS--SRVLKNTSRHPFLTSUKYFQTKDRLCFVMEYV	228	
Qy	117	NGGELPFHLQRERRFLEPRARFYAAVSAIGAIGVLSLNTIIRDLKPEINILLDCQGHVLT	176	
Db	229	NGGELPFHLSREVFSEDRTRFVGAEIVSALDYLHSGKIVYRDLKLENLMLDKDGHIKIT	288	
Qy	177	DFGLCKGEVPEDDTTTCGTPEYLAPEVLRKEPYDRAVDWNCGLAVLEMLHGLBPFFYS	236	
Db	289	DFGLCKEGITDAATMTKTCGTPEYLAPEVLENDNDYGRAVDWMLGVVYMYEMMCGRLFFYN	348	
Qy	237	QDVSYMYENILHQPLOIPGGRTVAACDLQLSKLLHKDQORL--GSKADFLEIKNHVFFSPI	295	

Db 349 QDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLIKDPNKRLLGGPPDDAKEIMRHSFFSGV 408
QY 296 NDDDLVHKRLTPFPNPNVGPADLKHDPDPFQEAIVSKISIGCTPDTVASSSGASSAFLGF 355
Db 409 NMQDVYDKLVLPFPKQVTSFTRFYDEFT-----AQTTITTP----- 448

QY 356 SYAPE--DDIILDC 367
Db 449 ---PEKYDEGDMDC 459

RESULT 12

US-09-771-161A-247
; Sequence 247, Application US/09771161A
; Patent No. 6936450

GENERAL INFORMATION:

; APPLICANT: LEVINE, et al.

; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES

; FILE REFERENCE: 802620-2005.1

; CURRENT APPLICATION NUMBER: US/09/771,161A

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 09/724,676

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 136776

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 135619

; PRIOR FILING DATE: 2000-04-12

; NUMBER OF SEQ ID NOS: 273

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 247

; LENGTH: 479

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-771-161A-247

Query Match 45.3%; Score 886; DB 2; Length 479;
Best Local Similarity 48.4%; Pred. No. 3.5e-79;
Matches 181; Conservative 55; Mismatches 100; Indels 38; Gaps 8;

QY 1 MNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDFLKVIQKGYGVLLAKRKS 56
Db 117 MNCSTP-----SQIDNIGEEEMDASTTHHKRKTWNDFYKLLGKGTGKVLVREKA 169
QY 57 DGAFYAVKVLQKKSILKKKEQSHMAERSVLLKNVHPFLGLRYSFQPEKLYFVLDYV 116
Db 170 SGKYAMKILKKEVIIAKDEVAHTLTE--SRVLKNTRHPELTSUKYSFQTKDRLCFVMEYV 228

QY 117 NGGELFFHLQRRERFLEPRARYAASAIQVLSLNIYYRDLKPEINILLDCQGHVLT 176
Db 229 NGGELFFHLRSRERVFSEDRTRFYGAIVSALDYLSHGKIVYRDLKLENMLDKDGHKIT 288

QY 177 DFGLCKEGVEPBDTSTFCGTPPEYLAPEVLRKEPDYRAVDWVCLGAVLYEMHLGLPPFYS 236
Db 289 DFGLCKEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDWVCLGAVLYEMHLGLPPFN 348

QY 237 QDVSWYENILHQPLOIPGGRVTAACDLQSLHLKQDQORL--GSKADFLEIKNHVFFSPI 295
Db 349 QDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLIKDPNKRLLGGPPDDAKEIMRHSFFSGV 408

QY 296 NDDDLVHKRLTPFPNPNVGPADLKHDPDPFQEAIVSKISIGCTPDTVASSSGASSAFLGF 355
Db 409 NMQDVYDKLVLPFPKQVTSFTRFYDEFT-----AQTTITTP----- 448

QY 356 SYAPE--DDIILDC 367

Db 449 ---PEKYDEGDMDC 459

RESULT 13

US-09-771-161A-248

; Sequence 248, Application US/09771161A

; Patent No. 6936450

; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.

; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES

; FILE REFERENCE: 802620-2005.1

; CURRENT APPLICATION NUMBER: US/09/771,161A

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 09/724,676

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 136776

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 135619

; PRIOR FILING DATE: 2000-04-12

; NUMBER OF SEQ ID NOS: 273

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 248

; LENGTH: 479

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-771-161A-248

Query Match 45.3%; Score 886; DB 2; Length 479;
Best Local Similarity 48.4%; Pred. No. 3.5e-79;
Matches 181; Conservative 55; Mismatches 100; Indels 38; Gaps 8;

QY 1 MNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDFLKVIQKGYGVLLAKRKS 56
Db 117 MNCSTP-----SQIDNIGEEEMDASTTHHKRKTWNDFYKLLGKGTGKVLVREKA 169
QY 57 DGAFYAVKVLQKKSILKKKEQSHMAERSVLLKNVHPFLGLRYSFQPEKLYFVLDYV 116
Db 170 SGKYAMKILKKEVIIAKDEVAHTLTE--SRVLKNTRHPELTSUKYSFQTKDRLCFVMEYV 228

QY 117 NGGELFFHLQRRERFLEPRARYAASAIQVLSLNIYYRDLKPEINILLDCQGHVLT 176
Db 229 NGGELFFHLRSRERVFSEDRTRFYGAIVSALDYLSHGKIVYRDLKLENMLDKDGHKIT 288

QY 177 DFGLCKEGVEPBDTSTFCGTPPEYLAPEVLRKEPDYRAVDWVCLGAVLYEMHLGLPPFYS 236
Db 289 DFGLCKEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDWVCLGAVLYEMHLGLPPFN 348

QY 237 QDVSWYENILHQPLOIPGGRVTAACDLQSLHLKQDQORL--GSKADFLEIKNHVFFSPI 295
Db 349 QDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLIKDPNKRLLGGPPDDAKEIMRHSFFSGV 408

QY 296 NDDDLVHKRLTPFPNPNVGPADLKHDPDPFQEAIVSKISIGCTPDTVASSSGASSAFLGF 355
Db 409 NMQDVYDKLVLPFPKQVTSFTRFYDEFT-----AQTTITTP----- 448

QY 356 SYAPE--DDIILDC 367

Db 449 ---PEKYDEGDMDC 459

RESULT 14

US-09-526-043-2

; Sequence 2, Application US/09526043

; Patent No. 6861555

GENERAL INFORMATION:

; APPLICANT: Guo, Kun

; APPLICANT: Pagnoni, Marco

; APPLICANT: Clark, Kenneth

; APPLICANT: Ivashchenko, Yuri

; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF

; FILE REFERENCE: A3278A-US

; CURRENT APPLICATION NUMBER: US/09/526,043

; CURRENT FILING DATE: 2000-03-14

; EARLIER APPLICATION NUMBER: 60/125,108

; EARLIER FILING DATE: 1999-03-19

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 465

; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-526-043-2

Query Match 45.0%; Score 878.5; DB 2; Length 465;
Best Local Similarity 51.0%; Pred. No. 1.9e-78;
Matches 172; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

QY 1 MNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDFLKVIKGNYGKVLAKRKS 56
Db 117 MNCSP-----SQIDNIGEEEMDASTTHKKKTWNDFYLLKLGKGTGKGVILVREKA 169
QY 57 DGAFYAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTPKLYFVLDYV 116
Db 170 SGKYAMKILKKEVIAKDEVAHTLTS-SRVLKNTRHPLTSLKYSFQIKDLRCFVMEYV 228
QY 117 NGGELFFHLQRRRFLPRARFYAAEVAASGIVLHSLNIIYDLKPNILLDCQGHVLT 176
Db 229 NGGELFFHLRSRERFSEDRTRFYGAIVSALDYLSGKIYVRLKLENMLDKDGHKIT 288
QY 177 DFGLCKEGVEPEDTTSTFCGTPYLAPVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYS 236
Db 289 DFGLCKEGITDAATMTKTCGTPYLAPVLENDYGRAVDWVGLGVVYEMMCGRLPFYN 348
QY 237 QVDSQMYENILHQLQIPGGRVTAACDILLQSLHKDQORL-GSKADFLEIKNHVFFSPI 295
Db 349 QDHEKLFELLMEDIKFPRTLSSDAKSLLSGLLIKDPNKRKLGCGPDDAKEIMRHSFFSGV 408
QY 296 NWDDLYHKRLTPFPNPNVTGPDADLKHDFDEFTQEAVS 332
Db 409 NWQDVYDKLVPPFKPQVTSETDTRYFDEEFTAQTTIT 445

RESULT 15

US-09-590-740-6
; Sequence 6, Application US/09590740
; Patent No. 6689807

; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-590-740-6

Query Match 45.0%; Score 878.5; DB 2; Length 480;
Best Local Similarity 47.8%; Pred. No. 1.9e-78;
Matches 175; Conservative 58; Mismatches 102; Indels 31; Gaps 7;

QY 6 AGTPSPQPSRANGNINLGPSANPNAQPT--DFDFLKVIKGNYGKVLAKRKSDFAYAV 63
Db 122 SGSPSDNSGAEEMVSL---AKPKHRVTWNEFEYLLKLGKGTGKGVILVKEKATGRYYAM 178
QY 64 KVLQKKSILKKKEQSHIMAEVSLLKNVRHPLVGLRYSFOTPEKLYFVLDVYNGGELFF 123
Db 179 KILKKEVIVAKDEVAHTLTENRV-LQNSRHPFLTALKYSFQTHDLRCFVMEYANGGELFF 237
QY 124 HLQRRRFLPRARFYAAEVAASGIVLHSLNIIYDLKPNILLDCQGHVLTDFGLCK 182
Db 238 HLSRERVFSEDRARFYGAIVSALDYLSHSEKNVYRDLKLENMLDKDGHKITDFGLCK 297
QY 183 EGVEPEDTTSTFCGTPYLAPVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSQDVSM 242
Db 298 EGKIDGATMTKTCGTPYLAPVLENDYGRAVDWVGLGVVYEMMCGRLPFYNQDHEKL 357
QY 243 YENILHQLQIPGGRVTAACDILLQSLHKDQORL-GSKADFLEIKNHVFFSPINWDDLY 301

Db 358 FELLIMEEIRFPTLGPFAKSLLSGLLKDDPTQRLGGSEDAKEIMQHRFFANIVWQDVT 417
QY 302 HKRLTPFPNPNVTGPDADLKHDFDEFTQEAVSIGCTPDVTVASSGASSAFLGFSYAPED 361
Db 418 EKKLSPPPKPVQVTSQDTRYFDEEFTAQMIT---ITP-----PDQ 454
QY 362 DDILDC 367
Db 455 DDSMEC 460

Search completed: January 27, 2006, 23:33:29
Job time : 19.3113 secs

; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 256
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-256

Query Match 100.0%; Score 1954; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120
QY 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240
DB 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240
QY 241 QMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORLGSKADFLKKNHVFSPINWDDL 300
DB 241 QMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORLGSKADFLKKNHVFSPINWDDL 300
QY 301 YHKRLTPPNPNVTGPDADLKHFDPEFTQEA VSKSIGCTPTDVASSSGASSAF LGFSYAPE 360
DB 301 YHKRLTPPNPNVTGPDADLKHFDPEFTQEA VSKSIGCTPTDVASSSGASSAF LGFSYAPE 360
QY 361 DDDILDC 367
DB 361 DDDILDC 367
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RESULT 5

US-10-380-235-6
; Sequence 6, Application US/10380235
; Publication No. US20040072184A1
; GENERAL INFORMATION:
; APPLICANT: Yoganathan, Thillainathan
; APPLICANT: Delaney, Allen
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND
; FILE REFERENCE: KINE-024CIP
; CURRENT APPLICATION NUMBER: US/10/380,235
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: IB01/02237
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/290,555
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/233,999
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,423
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/238,558
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-235-6

Query Match 100.0%; Score 1954; DB 4; Length 367;

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Best Local Similarity 100.0%; Pred. No. 1.1e-139;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60  
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
QY 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
DB 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240  
DB 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240  
QY 241 QMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORLGSKADFLKKNHVFSPINWDDL 300  
DB 241 QMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORLGSKADFLKKNHVFSPINWDDL 300  
QY 301 YHKRLTPPNPNVTGPDADLKHFDPEFTQEA VSKSIGCTPTDVASSSGASSAF LGFSYAPE 360  
DB 301 YHKRLTPPNPNVTGPDADLKHFDPEFTQEA VSKSIGCTPTDVASSSGASSAF LGFSYAPE 360  
QY 361 DDDILDC 367  
DB 361 DDDILDC 367
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RESULT 6

US-10-296-115-1109
; Sequence 1109, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1109
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1109

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Query Match 100.0%; Score 1954; DB 4; Length 382;  
Best Local Similarity 100.0%; Pred. No. 1.2e-139;  
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 16 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 75  
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 120  
DB 76 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYNGGE 135  
QY 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180  
DB 136 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 195  
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFYSDVS 240  
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QY 241 QMYENILHQPLOIPGGRVAAACDLSLLHKDQRLGSKADFLKKNHVFSPINWDDL 300
Db 256 QMYENILHQPLOIPGGRVAAACDLSLLHKDQRLGSKADFLKKNHVFSPINWDDL 315
QY 301 YHKRLTPPNVNTGPDADLKHFDPFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
Db 316 YHKRLTPPNVNTGPDADLKHFDPFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 375
QY 361 DDILDC 367
Db 376 DDILDC 382
RESULT 7
US-10-926-543-83
; Sequence 83, Application US/10926543
; Publication No. US20050048589A1
; GENERAL INFORMATION:
; APPLICANT: Jendoubi, Moncef
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCE, THEIR
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND DISEASE
; FILE REFERENCE: 705403.4004
; CURRENT APPLICATION NUMBER: US/10/926,543
; PRIOR FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US 60/497,790
; PRIOR FILING DATE: 2003-08-25
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-543-83
Query Match 100.0%; Score 1954; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.2e-139;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 30 MNSSPAGTSPQPSRANGNINLGPSANPNAOPTDFDLKVIKGNKGVKLLAKRSDGAF 89
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db 90 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 149
QY 121 LFFHLQRRERFLEPRARFYAAEVAASAIGYLHSLNIYRDLKPNILLLDCQGHVLTDFGL 180
Db 150 LFFHLQRRERFLEPRARFYAAEVAASAIGYLHSLNIYRDLKPNILLLDCQGHVLTDFGL 209
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPEDYDRAVDMWCLGAVLYEMHLGLPPFYSQDVS 240
Db 210 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPEDYDRAVDMWCLGAVLYEMHLGLPPFYSQDVS 269
QY 241 QMYENILHQPLOIPGGRVAAACDLSLLHKDQRLGSKADFLKKNHVFSPINWDDL 300
Db 270 QMYENILHQPLOIPGGRVAAACDLSLLHKDQRLGSKADFLKKNHVFSPINWDDL 329
QY 301 YHKRLTPPNVNTGPDADLKHFDPFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
Db 330 YHKRLTPPNVNTGPDADLKHFDPFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 389
QY 361 DDILDC 367
Db 390 DDILDC 396
RESULT 8
US-10-753-267-126
; Sequence 126, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
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; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriguez-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701.
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MPI03-003P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-126
Query Match 100.0%; Score 1954; DB 5; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.3e-139;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAOPTDFDLKVIKGNKGVKLLAKRSDGAF 60
Db 61 MNSSPAGTSPQPSRANGNINLGPSANPNAOPTDFDLKVIKGNKGVKLLAKRSDGAF 120
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 180
QY 121 LFFHLQRRERFLEPRARFYAAEVAASAIGYLHSLNIYRDLKPNILLLDCQGHVLTDFGL 180
Db 181 LFFHLQRRERFLEPRARFYAAEVAASAIGYLHSLNIYRDLKPNILLLDCQGHVLTDFGL 240
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPEDYDRAVDMWCLGAVLYEMHLGLPPFYSQDVS 240
Db 241 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPEDYDRAVDMWCLGAVLYEMHLGLPPFYSQDVS 300
QY 241 QMYENILHQPLOIPGGRVAAACDLSLLHKDQRLGSKADFLKKNHVFSPINWDDL 300
Db 301 QMYENILHQPLOIPGGRVAAACDLSLLHKDQRLGSKADFLKKNHVFSPINWDDL 360
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:31:20 ; Search time 64.3981 Seconds
(without alignments)
2381.178 Million cell updates/sec

Title: US-09-868-131A-1
Perfect score: 1954
Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFGLFSGYAPEDDILDC 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*
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- 4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1954	100.0	367	3	US-09-971-118-2
2	1954	100.0	367	4	US-10-291-172-256
3	1954	100.0	367	4	US-10-429-160-52
4	1954	100.0	367	4	US-10-221-278-256
5	1954	100.0	367	4	US-10-380-235-6
6	1954	100.0	382	4	US-10-296-115-1109
7	1954	100.0	396	5	US-10-926-543-83
8	1954	100.0	427	5	US-10-753-267-126
9	1767.5	90.5	398	4	US-10-262-511-140
10	1411	72.2	388	4	US-10-131-410-104
11	1411	72.2	407	4	US-10-067-977-4
12	1411	72.2	407	4	US-10-827-272-4
13	1411	72.2	431	3	US-09-981-353-7
14	1411	72.2	431	4	US-10-403-161-2
15	1411	72.2	431	4	US-10-403-161-4
16	1411	72.2	445	4	US-10-067-977-2
17	1411	72.2	445	4	US-10-827-272-2
18	1411	72.2	526	4	US-10-094-749-1861
19	1407	72.0	431	4	US-10-000-039-2
20	1407	72.0	431	4	US-10-353-690-12
21	1407	72.0	431	5	US-10-756-149-5279
22	1407	72.0	431	6	US-11-044-570-2
23	1404.5	71.9	430	3	US-09-810-808-9
24	1403	71.8	431	3	US-09-810-808-5
25	1392	71.2	594	5	US-10-732-923-10768
26	1390.5	71.2	433	5	US-10-732-923-10767
27	1342.5	68.7	340	4	US-10-217-574-17

28	1342.5	68.7	340	4	US-10-217-555-17	Sequence 17, Appl
29	1323.5	67.7	429	4	US-10-295-027-116	Sequence 116, Appl
30	1323.5	67.7	496	3	US-09-784-249-2	Sequence 2, Appli
31	1323.5	67.7	496	3	US-09-764-875-746	Sequence 746, App
32	1323.5	67.7	496	3	US-09-764-875-900	Sequence 900, App
33	1323.5	67.7	496	5	US-10-737-450-4	Sequence 4, Appli
34	1312.5	67.2	496	4	US-10-755-889-42	Sequence 42, Appl
35	1156.5	59.2	308	4	US-10-664-421-85	Sequence 85, Appl
36	1156.5	59.2	308	5	US-10-941-635-85	Sequence 85, Appl
37	983	50.3	422	4	US-10-369-493-7027	Sequence 7027, Ap
38	888.5	45.5	276	3	US-09-764-868-669	Sequence 669, App
39	888.5	45.5	276	3	US-09-764-875-1176	Sequence 1176, Ap
40	886	45.3	479	3	US-09-771-161A-246	Sequence 246, App
41	886	45.3	479	3	US-09-771-161A-247	Sequence 247, App
42	886	45.3	479	3	US-09-771-161A-248	Sequence 248, App
43	886	45.3	479	4	US-10-394-322A-3	Sequence 3, Appli
44	886	45.3	479	4	US-10-217-574-33	Sequence 33, Appl
45	886	45.3	479	4	US-10-217-555-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-09-971-118-2
; Sequence 2, Application US/09971118
; Patent No. US20020123056A1
; GENERAL INFORMATION:
; APPLICANT: DELANEY, ALLEN
; APPLICANT: YOGANATHAN, THILLAINATHAN
; TITLE OF INVENTION: SGK2 AND ITS USES
; FILE REFERENCE: KINE025CIP
; CURRENT APPLICATION NUMBER: US/09/971,118
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/21479
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-118-2

Query Match	100.0%;	Score	1954;	DB	3;	Length	367;
Best Local Similarity	100.0%;	Pred. No.	1.1e-139;				
Matches	367;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MNSSPAGTSPQPSRANGNINIGPSANPNAQTD	DFDLKVIGKNGYKVLAKRKS	SDGAF	60		
Db	1	MNSSPAGTSPQPSRANGNINIGPSANPNAQTD	DFDLKVIGKNGYKVLAKRKS	SDGAF	60		
QY	61	YAVKVLQKKSILKKEQSHIMAEVSVLLKNVRHPLVGLRYSFQ	TEPEKLYFVLDVYNGE	120			
Db	61	YAVKVLQKKSILKKEQSHIMAEVSVLLKNVRHPLVGLRYSFQ	TEPEKLYFVLDVYNGE	120			
QY	121	LFPHLQRRRFLPEPRFYAAEVA	SAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL	180			
Db	121	LFPHLQRRRFLPEPRFYAAEVA	SAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL	180			
QY	181	CKEGVEPEDTSTFCGTPEYLAPEVLRKEPYDRADVW	WCLGAVLYEMLHGLPPFYSQDVS	240			
Db	181	CKEGVEPEDTSTFCGTPEYLAPEVLRKEPYDRADVW	WCLGAVLYEMLHGLPPFYSQDVS	240			
QY	241	QMYENILHQPLOIPGRTVAACDL	LQSLHKDQORLGSKADFLEIKNHVFPSPINWDDL	300			
Db	241	QMYENILHQPLOIPGRTVAACDL	LQSLHKDQORLGSKADFLEIKNHVFPSPINWDDL	300			
QY	301	YHKRLTPFPNPNVTGPADLKHFDPDFTQ	BAVSKSGICCTPDTVASSSGASSAFGLF	360			
Db	301	YHKRLTPFPNPNVTGPADLKHFDPDFTQ	BAVSKSGICCTPDTVASSSGASSAFGLF	360			

QY 361 DDDILDC 367
Db 361 DDDILDC 367

RESULT 2

US-10-291-172-256
; Sequence 256, Application US/10291172
; Publication No. US20030228584A1

GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 256
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-256

Query Match 100.0%; Score 1954; DB 4; Length 367;

Best Local Similarity 100.0%; Pred. No. 1.1e-139; Mismatches 0; Indels 0; Gaps 0;
Matches 367; Conservative 0;

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|||||
61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
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121 LFFHLQRRERFLEPRARFYAAEVAASAI GYLHLSNIIYRDLKPENILLDCQGHVLTDFGL 180
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|||||
241 QMYENILHQPLOIPGGRITVAACDLLQSLHKKDQRLGSKADFLFIKNHVFSPINWDDL 300
301 YHKRLTPPNPNVTGPADLKHPDPTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
|||||
301 YHKRLTPPNPNVTGPADLKHPDPTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
361 DDDILDC 367
361 DDDILDC 367

RESULT 3

US-10-429-160-52
; Sequence 52, Application US/10429160
; Publication No. US20040023276A1

GENERAL INFORMATION:

; APPLICANT: Ward, Teresa R
; APPLICANT: Mao, Mao
; APPLICANT: Linsley, Peter S
; APPLICANT: Lund, Lund
; TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
; FILE REFERENCE: RS0200
; CURRENT APPLICATION NUMBER: US/10/429,160
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/377,714
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-160-52

Query Match 100.0%; Score 1954; DB 4; Length 367;

Best Local Similarity 100.0%; Pred. No. 1.1e-139; Mismatches 0; Indels 0; Gaps 0;
Matches 367; Conservative 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60
|||||
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60
61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
|||||
61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
121 LFFHLQRRERFLEPRARFYAAEVAASAI GYLHLSNIIYRDLKPENILLDCQGHVLTDFGL 180
|||||
121 LFFHLQRRERFLEPRARFYAAEVAASAI GYLHLSNIIYRDLKPENILLDCQGHVLTDFGL 180
181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSQDYS 240
|||||
181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEPYDRAVDWCLGAVLYEMLHGLPPFYSQDYS 240
241 QMYENILHQPLOIPGGRITVAACDLLQSLHKKDQRLGSKADFLFIKNHVFSPINWDDL 300
|||||
241 QMYENILHQPLOIPGGRITVAACDLLQSLHKKDQRLGSKADFLFIKNHVFSPINWDDL 300
301 YHKRLTPPNPNVTGPADLKHPDPTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
|||||
301 YHKRLTPPNPNVTGPADLKHPDPTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
361 DDDILDC 367
361 DDDILDC 367

RESULT 4

US-10-221-278-256

; Sequence 256, Application US/10221278
; Publication No. US20040034208A1

GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07

QY 301 YHRLTPPNVNTGADLKHDFPTEQAVSKSIGCTPTVASSGSAFLGFSYAPE 360
Db 361 YHRLTPPNVNTGADLKHDFPTEQAVSKSIGCTPTVASSGSAFLGFSYAPE 420
QY 361 DDILDC 367
Db 421 DDILDC 427

RESULT 9

US-10-262-511-140
; Sequence 140, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Raftelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqdist version 0.1
; SEQ ID NO 140
; LENGTH: 398
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-262-511-140
Query Match 90.5%; Score 1767.5; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 1.6e-125;
Matches 338; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MNSSPACTSPQPSRANGNINLGPSANPNAQPTDFDLKVIGKNGYKVLAKRKS DGAF 60
Db 61 MNSSPACTSPQPSRANGNINLGPSANPNAQPTDFDLKVIGKNGYKVLAKRKS DGAF 120
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 180
QY 121 LEPHLQRRERFLEPRARFYAAEVAESAIGVLSHLSNIIYRDLKPENILLDCQHVVLDTDFGL 180
Db 181 LEPHLQRRERFLEPRARFYAAEVAESAIGVLSHLSNIIYRDLKPENILLDCQ----- 230
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEPYDRAVDWMCIGAVLYEMLHGLRPPFYSQDVS 240
Db 231 -----YLAPEVLKPEPYDRAVDWMCIGAVLYEMLHGLRPPFYSQDVS 271
QY 241 QMYENILHQLOIPGGRTVAAACDLQLSLHKKQORQLGSKADFLKIKNVHFFSPINWDDL 300
Db 272 QMYENILHQLOIPGGRTVAAACDLQLSLHKKQORQLGSKADFLKIKNVHFFSPINWDDL 331
QY 301 YHRLTPPNVNTGADLKHDFPTEQAVSKSIGCTPTVASSGSAFLGFSYAPE 360
Db 332 YHRLTPPNVNTGADLKHDFPTEQAVSKSIGCTPTVASSGSAFLGFSYAPE 391
QY 361 DDILDC 367
Db 392 DDILDC 398

RESULT 10

US-10-131-410-104
; Sequence 104, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-104
Query Match 72.2%; Score 1411; DB 4; Length 388;
Best Local Similarity 71.2%; Pred. No. 1.5e-98;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;
QY 1 MNSSPACTSPQPSRANGNINLGPSANPNAQPTDFDLKVIGKNGYKVLAKRKS DGAF 60
Db 26 MNANP--SPPPSPSQ---QINLGPSNPHAKSDPHFLKVIGKSGFGLARHKAEEVF 80
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120

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Db      81 YAVKVLQKXKLLKKKEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVDYNGGE 140
QY      121 LFFHLQRRERFLPRARFVAEEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db      141 LFFHLQRRERFLPRARFVAEEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 200
QY      181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKRPDYRAVDWVWCLGAVLYEMLHGLPFPYSQDVS 240
Db      201 KENIEHNHTTSTFCGTPPEYLAPEVLKRPDYRTDWMCLGAVLYEMLYGLPFPYSRNTA 260
QY      241 QMYENILHQPLOIPGGRTVAAACDLQLSLHDKQORLGSKADPFLKKNHVFSPINWDDL 300
Db      261 EMYDNLNKLPLQKPNITNSARHLLGLLQKTRKLGAKDDFMEIKSHVFFSLINWDDL 320
QY      301 YHKRLTPPNPNVNTGPDADLKHFDPFTQBAVSKSIGCTPDTV---ASSSGASSAFILGFSY 357
Db      321 INKKITPPPNPNVSGNDLRHDFDPTFEPVPNSIGKSPDSVLVTASVKEAAEAFILGFSY 380
QY      358 APEDDDIL 365
Db      381 APPTDSFL 388
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RESULT 11
US-10-067-977-4
; Sequence 4, Application US/10067977
; Publication No. US20030157679A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-4
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Query Match      72.2%; Score 1411; DB 4; Length 407;
Best Local Similarity 71.2%; Pred. No. 1.6e-98;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

QY      1 MNSSPAGTSPQSPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
Db      45 MNANP--SPPPSPSQ---QINLGPSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVF 99
QY      61 YAVKVLQKXKLLKKKEQHSHMAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLVDYNGGE 120
Db      100 YAVKVLQKXKLLKKKEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVDYNGGE 159
QY      121 LFFHLQRRERFLPRARFVAEEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db      160 LFFHLQRRERFLPRARFVAEEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 219
QY      181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKRPDYRAVDWVWCLGAVLYEMLHGLPFPYSQDVS 240
Db      220 KENIEHNHTTSTFCGTPPEYLAPEVLKRPDYRTDWMCLGAVLYEMLYGLPFPYSRNTA 279
QY      241 QMYENILHQPLOIPGGRTVAAACDLQLSLHDKQORLGSKADPFLKKNHVFSPINWDDL 300
Db      280 EMYDNLNKLPLQKPNITNSARHLLGLLQKTRKLGAKDDFMEIKSHVFFSLINWDDL 339
QY      301 YHKRLTPPNPNVNTGPDADLKHFDPFTQBAVSKSIGCTPDTV---ASSSGASSAFILGFSY 357
Db      340 INKKITPPPNPNVSGNDLRHDFDPTFEPVPNSIGKSPDSVLVTASVKEAAEAFILGFSY 399
QY      358 APEDDDIL 365
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Db      400 APPTDSFL 407

RESULT 12
US-10-827-272-4
; Sequence 4, Application US/10827272
; Publication No. US20040203127A1
; GENERAL INFORMATION:
; APPLICANT: KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL001313-DIV
; CURRENT APPLICATION NUMBER: US/10/827,272
; CURRENT FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-827-272-4

Query Match      72.2%; Score 1411; DB 4; Length 407;
Best Local Similarity 71.2%; Pred. No. 1.6e-98;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

QY      1 MNSSPAGTSPQSPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
Db      45 MNANP--SPPPSPSQ---QINLGPSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVF 99
QY      61 YAVKVLQKXKLLKKKEQHSHMAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLVDYNGGE 120
Db      100 YAVKVLQKXKLLKKKEKHMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLVDYNGGE 159
QY      121 LFFHLQRRERFLPRARFVAEEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db      160 LFFHLQRRERFLPRARFVAEEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 219
QY      181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKRPDYRAVDWVWCLGAVLYEMLHGLPFPYSQDVS 240
Db      220 KENIEHNHTTSTFCGTPPEYLAPEVLKRPDYRTDWMCLGAVLYEMLYGLPFPYSRNTA 279
QY      241 QMYENILHQPLOIPGGRTVAAACDLQLSLHDKQORLGSKADPFLKKNHVFSPINWDDL 300
Db      280 EMYDNLNKLPLQKPNITNSARHLLGLLQKTRKLGAKDDFMEIKSHVFFSLINWDDL 339
QY      301 YHKRLTPPNPNVNTGPDADLKHFDPFTQBAVSKSIGCTPDTV---ASSSGASSAFILGFSY 357
Db      340 INKKITPPPNPNVSGNDLRHDFDPTFEPVPNSIGKSPDSVLVTASVKEAAEAFILGFSY 399
QY      358 APEDDDIL 365
Db      400 APPTDSFL 407

RESULT 13
US-09-981-353-7
; Sequence 7, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 431
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1
US-09-981-353-7

Query Match          72.2%; Score 1411; DB 3; Length 431;
Best Local Similarity 71.2%; Pred. No. 1.7e-98;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

Qy 1 MNSSPAGTSPQPSRANGNINLGPSANPNQAOTDFDLKVIGKNGYGVLLAKRKSDGAF 60
Db 69 MNANP--SPPPSPSQ--QINLGSPSNPHAKPSDFHLKVIGKSGFGKVLARHKAEEVF 123
Qy 61 YAVKVLQKSTILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLIDYNGGE 120
Db 124 YAVKVLQKKAAILKKKEKHIMSERNVLLKNVRHPFLVGLHFSFQTADKLYFVLIDYNGGE 183
Qy 121 LFPHLQRRERFLEPRARFYAAEASAIYGLHSLNIIYRDLKPENILLDCQGHVVLDTDFGL 180
Db 184 LFVHLQRCERCFLEPRARFYAAETASALGYLHSLNIVYRDLKPENILLDSQGHIVLDTDFGL 243
Qy 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDVS 240
Db 244 CKENIEHNSTTSTFCGTPPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA 303
Qy 241 QMVENILHQLPQTGGRTVAACDQLLSLLHKDQRLGSKADFLKIKNVHFFSPINWDDL 300
Db 304 EMDYDNLNKLPLQKPNITNSARHLLGLELLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDL 363
Qy 301 YHKRLTPPPNPVNTGPAHLKHDFEFTQEAVSXKSIGCTPDTV--ASSSCASSAFLGFSY 357
Db 364 INKKTIPFPNPNVSGPNDLRHDFEFTPEEPVPNSIGKSPDSVLVTASVKEAAEAFGLGFSY 423
Qy 358 APEDDDIL 365
Db 424 APPTDSFL 431

RESULT 14
US-10-403-161-2
; Sequence 2, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2

; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-2

Query Match          72.2%; Score 1411; DB 4; Length 431;
Best Local Similarity 71.2%; Pred. No. 1.7e-98;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

Qy 1 MNSSPAGTSPQPSRANGNINLGPSANPNQAOTDFDLKVIGKNGYGVLLAKRKSDGAF 60
Db 69 MNANP--SPPPSPSQ--QINLGSPSNPHAKPSDFHLKVIGKSGFGKVLARHKAEEVF 123
Qy 61 YAVKVLQKSTILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLIDYNGGE 120
Db 124 YAVKVLQKKAAILKKKEKHIMSERNVLLKNVRHPFLVGLHFSFQTADKLYFVLIDYNGGE 183
Qy 121 LFPHLQRRERFLEPRARFYAAEASAIYGLHSLNIIYRDLKPENILLDCQGHVVLDTDFGL 180
Db 184 LFVHLQRCERCFLEPRARFYAAETASALGYLHSLNIVYRDLKPENILLDSQGHIVLDTDFGL 243
Qy 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDVS 240
Db 244 CKENIEHNSTTSTFCGTPPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA 303
Qy 241 QMVENILHQLPQTGGRTVAACDQLLSLLHKDQRLGSKADFLKIKNVHFFSPINWDDL 300
Db 304 EMDYDNLNKLPLQKPNITNSARHLLGLELLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDL 363
Qy 301 YHKRLTPPPNPVNTGPAHLKHDFEFTQEAVSXKSIGCTPDTV--ASSSCASSAFLGFSY 357
Db 364 INKKTIPFPNPNVSGPNDLRHDFEFTPEEPVPNSIGKSPDSVLVTASVKEAAEAFGLGFSY 423
Qy 358 APEDDDIL 365
Db 424 APPTDSFL 431

RESULT 15
US-10-403-161-4
; Sequence 4, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 431
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:32:16 ; Search time 9.46352 Seconds
(without alignments)
419.957 Million cell updates/sec

Title: US-09-868-131A-1

Perfect score: 1954

Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFLGFSYAPEDDDILDC 367

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB_PEP.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB_PEP.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB_PEP.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB_PEP.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB_PEP.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1411	72.2	543	US-10-821-234-1158	Sequence 1158, Ap
2	874.5	44.8	480	US-11-109-156-18	Sequence 18, Appl
3	788.5	40.4	495	US-10-770-726-81	Sequence 81, Appl
4	761	38.9	737	US-11-152-366-28	Sequence 28, Appl
5	722.5	37.0	740	US-10-878-556A-129	Sequence 129, App
6	705.5	36.1	341	US-11-092-168-4	Sequence 4, Appli
7	701.5	35.9	942	US-10-770-726-76	Sequence 76, Appl
8	694.5	35.5	343	US-11-092-168-3	Sequence 3, Appli
9	694.5	35.5	351	US-11-132-142-13	Sequence 13, Appl
10	691.5	35.4	351	US-11-132-142-14	Sequence 14, Appl
11	690.5	35.3	462	US-11-132-142-10	Sequence 10, Appl
12	681.5	34.9	350	US-10-497-767-9	Sequence 9, Appli
13	681.5	34.9	381	US-11-132-142-9	Sequence 9, Appli
14	681	34.9	705	US-10-995-561-856	Sequence 856, App
15	681	34.9	706	US-10-995-561-855	Sequence 855, App
16	681	34.9	706	US-11-099-958-1	Sequence 1, Appli
17	679	34.7	351	US-11-099-958-2	Sequence 2, Appli
18	675	34.5	353	US-11-132-142-11	Sequence 11, Appl
19	672.5	34.4	395	US-11-132-142-12	Sequence 12, Appl
20	670	34.3	515	US-11-132-142-8	Sequence 8, Appli
21	662	33.9	398	US-11-132-142-7	Sequence 7, Appli
22	649.5	33.2	548	US-11-132-142-5	Sequence 5, Appli
23	644	33.0	480	US-11-132-142-6	Sequence 6, Appli
24	547	28.0	637	US-11-113-837-4	Sequence 4, Appli
25	541.5	27.7	1732	US-10-055-877-147	Sequence 147, App

ALIGNMENTS

RESULT 1

US-10-821-234-1158
; Sequence 1158, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1158
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1158

Query Match 72.2%; Score 1411; DB 6; Length 543;
Best Local Similarity 71.2%; Pred. No. 1e-121;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

QY 1 MNSSPAGTSPQPSRANGNINIGPSANPAQPTDFDLKVIKGNYGKVLAKRKS DGAF 60
Db 181 MNANP-SPPSPSQ--QINLGPSNPHAKSPDFHLKVIKGSFGKVLARHKAEEVF 235

QY 61 YAVKLOKSLKKEQSHMAERSVLKNVPHFLVGLRYFQPEKLYFVLDVYNGGE 120
Db 236 YAVKYLQKAILKKEEKHIMSERNVLLKNVHFLVGLHFLSFQADKLYFVLDVINGGE 295

QY 121 LFFHLQRRERFLPRARFYAAEVAISAIGVLHSLNIIYRDLPENILLDCQGHVLTDFGL 180
Db 296 LFYHLQRECFLEPRARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHVLTDFGL 355

QY 181 CKGEVEPDTTSTFCGTPEYLAPEVLRKEPYDRAVDWMLGAVLYEMLHGLPPFPYSQDVS 240
Db 356 CKENIEHNSTSTFCGTPEYLAPEVLRKEPYDRTDWMCLGAVLYEMLYGLPFPYSRNTA 415

QY 241 QYENILHQPLQIPGRTVAACDILLOSLLHKDQORLQSKADFLKHNHVFSPINWDDL 300
Db 416 EMYDNLNKLQKPNITNSARHLLLEGLLQKDRTRLGAKDPMFKSHVFPFSLINWDDL 475

QY 301 YHKRLTPFPNPNVTGPADLKHFPDPTQEAVSKSIGCTPDVT---ASSSGASSAFLGFSY 357

Db 476 INKKTTPPNPNVSGNDLRHDPFTEEPVNSIGKSDPSVLVITASVKEAAEAFLGFSY 535

Qy 358 APEDDIL 365

Db 536 APPTDSFL 543

RESULT 2

US-11-109-156-18

; Sequence 18, Application US/11109156

; Publication No. US20050250144A1

; GENERAL INFORMATION:

; APPLICANT: Toehio Ota

; APPLICANT: Takao Isogai

; APPLICANT: Tetsuo Nishikawa

; APPLICANT: Koji Hayashi

; APPLICANT: Kaoru Otsuka

; APPLICANT: Jun-Ichi Yamamoto

; APPLICANT: Shizuko Ishii

; APPLICANT: Tomoyasu Sugiyama

; APPLICANT: Ai Wakamatsu

; APPLICANT: Keiichi Nagai

; APPLICANT: Tetsuji Otsuki

; APPLICANT: Shin-Ichi Funahashi

; APPLICANT: Chiaki Senoo

; APPLICANT: Jun-Ichi Nezu

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN

; TITLE OF INVENTION: PHOSPHATASE

; FILE REFERENCE: 06501-099002

; CURRENT APPLICATION NUMBER: US/11/109,156

; CURRENT FILING DATE: 2005-04-19

; PRIOR APPLICATION NUMBER: US/10/060,065

; PRIOR FILING DATE: 2002-01-29

; PRIOR APPLICATION NUMBER: PCT/JP06/05061

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/159,590

; PRIOR FILING DATE: 1999-10-18

; PRIOR APPLICATION NUMBER: US 60/183,322

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: JP 11-248036

; PRIOR FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: JP 2000-118776

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: JP 2000-183767

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: JP 2000-241899

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 18

; LENGTH: 480

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-109-156-18

Query Match 44.8%; Score 874.5; DB 7; Length 480;

Best Local Similarity 47.5%; Pred. No. 1.3e-72;

Matches 174; Conservative 59; Mismatches 102; Indels 31; Gaps 7;

Qy 6 AGTPSPQPSRANGNINLGSANPNAOPT--DQDFLVKVGKNGYKVLAKRKSDDGAFYAV 63

Db 122 SGSPSDNSGAEMEVSLS--AKPKHRTVTNFEYLLKLGKGTGKVLVKEKATGRYAM 178

Qy 64 KVLQKSLKKGKQSHIMAERSVLLKNVRHPPFLVGLRYSFQTEPKLYFVLVDYVNGGELFF 123

Db 179 KILKKEVIKAKDVAITLTENRV-LQNSRHPPFLTALKYSFQTHDRUCFVNEVANGELFF 237

Qy 124 HLQRRERFLPRARFYAAEASAIYGLHS-LNIIYRDLPENILLDCQGHVVLTDGFLCK 182

Db 238 HLSRERFVSDRARFYGAETVSALDYLHSEKNVVYRDLENLMLDKGHIKITDFGLCK 297

Qy 183 EGVPEPDTTSTFCGTEPYLAPEVRKEPYDRVDWVCLGAVLYEMLHGLPPFYSDVSQM 242

Db 298 EGKDGATMKTFCTGTEPYLAPEVLEDNDYGRAVDWVGLGVVYEMWCGRLPFYNQDHEKL 357

Qy 243 YENILHQPIQPGGRTVAACDLLOSLLHKDQORL-GSKADFLFIKNHVFFSPINWDDLY 301

Db 358 FELILMEIRFPRTLGPPEAKSLLSGLLKDKPKQRLGGGSEDAKEIMQHRFFAGIVQHVY 417

Qy 302 HKRLTPPNPNVTGPADLKHDPPEPTQEAUSKSICTPDTVASSSGASSAFILGFSVAPED 361

Db 418 EKKUSPPFKPQVTSMTDTRYDDEFTAQMIT----ITP-----PQ 454

Qy 362 DDILDC 367

Db 455 DDSMEC 460

RESULT 3

US-10-770-726-81

; Sequence 81, Application US/10770726

; Publication No. US20050266409A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Brown, Eugene

; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

; TITLE OF INVENTION: CANCERS

; FILE REFERENCE: AM101079 (031896-010000)

; CURRENT APPLICATION NUMBER: US/10/770,726

; CURRENT FILING DATE: 2004-02-04

; NUMBER OF SEQ ID NOS: 48640

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 81

; LENGTH: 495

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-770-726-81

Query Match 40.4%; Score 788.5; DB 6; Length 495;

Best Local Similarity 45.8%; Pred. No. 1.1e-64;

Matches 162; Conservative 64; Mismatches 111; Indels 17; Gaps 8;

Qy 19 NINLGPSANPNAOPTDQDFLVKVGKNGYKVLAKRKSDD--GAFYAVKVLQKSLK-- 74

Db 67 SVNVGPE--RIGPHCFELLRVLGKGYKVFQVRKVQGTNLGKIYAMKVLKAKIVRNA 123

Qy 75 KEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTEPKLYFVLVDYVNGGELFFHLQRRERFLP 134

Db 124 KDTAHTRAERNI-LESVKHPFIVELAYAFQTGGKLYLILECLSGGELFTHLEREGIFLED 182

Qy 135 RARFYAAEASAIYGLHS-LNIIYRDLPENILLDCQGHVVLTDGFLCKEGVEPEDTTSF 194

Db 183 TACFYLAETITLALGHLHSGIIYRDLPENIMLSQGHKLTDFGLCKESIHEGAVHTF 242

Qy 195 CGTEPYLAPEVRKEPYDRVDWVCLGAVLYEMLHGLPPFYSDVSQVSYENILHQPIQ 254

Db 243 CGTIEYMAPEILVRSCHNRADVNSLGMVDMLTGSPPTAENKKTWDKILRGKALP 302

Qy 255 GORTVAACDLLOSLLHKDQORL-GSKADFLFIKNHVFFSPINWDDLYHKRLTPTPPNPNV 313

Db 303 PYLTPDARDLVKFLKRNPSQRIGGPGDAADVQRHPPFRHNMWDDLLAWRVDPPRPCL 362

Qy 314 TGPADLKHDPPEPTQEAUSKSICTPDTVASSSGASSAFILGFSY-APEDDDILD 366

Db 363 QSEEDVSQDTRFTTRQTPVDS----PDDTALSESANQAFLGFTYVAP---SVLD 409

RESULT 4

US-11-152-366-28

; Sequence 28, Application US/11152366

; Publication No. US20060014184A1

; GENERAL INFORMATION:

; APPLICANT: Brys, Reginald

; APPLICANT: Vandeghinste, Nick

:	APPLICANT:	Tohme, Peter H. M.			
:	TITLE OF INVENTION:	Methods For Identification, And Compounds Useful For The			
:	TITLE OF INVENTION:	Treatment Of Degenerative & Inflammatory Diseases			
:	FILE REFERENCE:	P27,680-A USA			
:	CURRENT APPLICATION NUMBER:	US/11/152,366			
:	CURRENT FILING DATE:	2005-06-14			
:	PRIOR APPLICATION NUMBER:	60/579,307			
:	PRIOR FILING DATE:	2004-06-14			
:	NUMBER OF SEQ ID NOS:	295			
:	SOFTWARE:	PatentIn version 3.3			
:	SEQ ID NO 28				
:	LENGTH:	737			
:	TYPE:	PRT			
:	ORGANISM:	Homo sapiens			
:	US-11-152-366-28				
	Query Match	38.9%; Score 761; DB 7; Length 737;			
	Best Local Similarity	42.5%; Pred.No. 6e-62;			
	Matches	158; Conservative 66; Mismatches 118; Indels 30; Gaps 6;			
Qy	3 SSPAG-TSPSQSRANGNINLGPSANPNAOFTDFDLKVIKGNGYKVLLAKRKSDGAFY	61			
Dd	380 SSPDGLQMLSP--GENGEVRQGQAIRGLGD--SENFIKVLGKSFGVKWLAELKGRDEVY	434			
Qy	62 AVKVLQKKSLILKKKEQHSHIMAEBSVLLKNVRHPLVGLRYSFOTPEKLIFVLDDVYNGEL	121			
Dd	435 AVKVLKDDVLPVWLTSKEAVSILKAPMTKNPHKRLGCVASQNGEDAICKQHPFFKEIDMW	494			
Qy	122 FFHLQRERRELEPRAREYAAEVAISAICYIHSLNIIYRDLPENILLDCQGHVLTDPGLC	181			
Dd	495 MFQIQRSRKEDEPRSRFYAAEVTSALMFLHQGVIVYRDLKLDNLILDAGECHKLADFGMC	554			
Qy	182 KEQVEPEDTTSTFCGTPEYLAPLVLRKEPYDRADVMMCLGAVLYEMLHGLPPFVSQDVQS	241			
Dd	555 KEGILGNVTITTCGTPDYIAPIILQLEYCPSPVDWWALGVLYEMMAGQPPEADNEDD	614			
Qy	242 MYENILHQPILQIPGGRTVAACDLLQLSKHKDQORLG---SKADFLEIKNHVPFPINWD	298			
Dd	615 LFESILHDDVLYPVWLTSKEAVSILKAPMTKNPHKRLGCVASQNGEDAICKQHPFFKEIDMW	674			
Qy	299 DLXHKRLTTPFNPNVTCGPADLKHFDEPTQ-----EAVSKSIGCTPDTVASSSGAS	349			
Dd	675 LLEQKIKPKPRIKITKRDNVNFDODFTREEPVLTLVDEAIVKQIN-----Q 722				
Qy	350 SAFLGFSYAPED 361				
Dd	723 EEFKGFSYGED 734				
RESULT 5					
US-10-878-556A-129					
:	Sequence	129, Application US/10878556A			
:	Publication No.	US20050266399A1			
:	GENERAL INFORMATION:				
:	APPLICANT:	Hoffmann La-Roche Inc.			
:	TITLE OF INVENTION:	HCV regulated protein expression			
:	FILE REFERENCE:	21762			
:	CURRENT APPLICATION NUMBER:	US/10/878,556A			
:	CURRENT FILING DATE:	2004-06-28			
:	NUMBER OF SEQ ID NOS:	199			
:	SOFTWARE:	PatentIn version 3.1			
:	SEQ ID NO 129				
:	LENGTH:	740			
:	TYPE:	PRT			
:	ORGANISM:	Homo sapiens			
:	PUBLICATION INFORMATION:				
:	DATABASE ACCESSION NUMBER:	sw_hum/k6a3_human			
:	DATABASE ENTRY DATE:	1996-10-01			
:	US-10-878-556A-129				
	Query Match	37.0%; Score 722.5; DB 6; Length 740;			
	Best Local Similarity	44.4%; Pred.No. 2e-58;			
	Matches	151; Conservative 58; Mismatches 118; Indels 13; Gaps 6;			

Db 83 KRI-LQAVNFPFLVLEFSGKNSLYMVEYVAGGEMFSLHURIGRFAEPHARFYAAQI 141
QY 144 ASAGYLHSLNIYRDLPENILDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPEYLAP 203
Db 142 VLTFEYLHSLDIYRDLPENILDCQGVYQVTDGFAK--RVKGRWTWLCGTPEYLAP 198
QY 204 EVLRKEPYDRAVDWCLGAVLYEMHLGLPPFYSQDSQMYENILHQLPQIPGGRVAACD 263
Db 199 EILSKGYNKAVDMMWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFPFHSDDLKD 258
QY 264 LLOSLHKKDQORLGS-KADFLKHNHVFSPINWDDLHYKRLTPFPNPNVVTGPADLKH 322
Db 259 LURNLLQVLTFRKGNLKGNDIKNHWFAITDIAIYQKVEAPFIPKFGPGDTSNF 318
QY 323 DPEFTQEAIVSKI 335
Db 319 D-DYEEIEIRVSI 330
RESULT 7
US-10-770-726-76
; Sequence 76, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-76
Query Match 35.9%; Score 701.5; DB 6; Length 942;
Best Local Similarity 40.7%; Pred. No. 2.4e-56;
Matches 154; Conservative 65; Mismatches 124; Indels 35; Gaps 8;
QY 3 SSPAGTSP-QPSRANGNINLGPSANPNAQPT-----PELPSETQETPGPALCSPLRKSPLTLEDFKFLAVLGRG 624
Db 572 SSPSSLSPIQESTA-----PELPSETQETPGPALCSPLRKSPLTLEDFKFLAVLGRG 624
QY 45 NYGKVLAKKSDCAFYAVKVLQKKSILKKKQSHMAERSVL--LKNVRHFPVLGLRYS 102
Db 625 HFGKVLSSFRPSGELFAIKALKKGDIVARDEVESLMCEKRIILAAVTSAGHPPLVNLFGC 684
QY 103 FOTPEKLYFVLDVYNGGELFFHLQRRRRFLPRARFYAAEVAASAIGYLHSLNIYRDLPK 162
Db 685 FQTPPEHVCVFMEVSAAGDMLHLHSD-VFSEPAIFYSACVLGLQFLHEHKIYRDCLK 743
QY 163 ENILLDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPEYLAPEYLRKEPYDRAVDWVWCLGA 222
Db 744 DNLLLDTEGVKVIADFGLCCKEGYGDRTSTFCGTPEFLAPEVLTDTSTRAVDWVWGLGV 803
QY 223 VLYEMHLGLPPFYSQDSQMYENILHQLPQIPGGRVAACDLLOSLHKKDQORLG-SKA 281
Db 804 LLYEMLVGSPPFGDDEEVFOSVNDVRYRFLSAAEIGIMRLLRNPRLGSSR 863
QY 282 DFLEIKHNHVFSPINWDDLHYKRLTPFPNPNVVTGPADLKHDFEFTQEA--VSKSIGCTP 339
Db 864 DAEVKKQPFRTGLGWEALLARKLPFPFVTLTSGRTDVSNFDEEFTGEAPTLSPPRDAR 923
QY 340 DTVASSSSGSAFLGFSY 357
Db 924 LTAAE---QAFLDFDF 937

RESULT 8
US-11-092-168-3
; Sequence 3, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bearss, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-092-168-3
Query Match 35.5%; Score 694.5; DB 7; Length 343;
Best Local Similarity 43.1%; Pred. No. 2.6e-56;
Matches 135; Conservative 66; Mismatches 105; Indels 7; Gaps 5;
QY 24 PSANPNAPQTPDFKLVKVGKNGYKVLAKRKSDFAVKVLQKKSILKKKEQSHIMAE 83
Db 26 PAQN-TAHLDDQPERIKTLGTSGFGRVMLVKHKETGNHFAMKILDQKVVYKLAQIEHTLNE 84
QY 84 RSVLLKNVRHPPVLGLRYSFOTPEKLYFVLDVYNGGELFFHLQRRRRFLPRARFYAAEV 143
Db 85 KRI-LQAVNFPFLVLEFSGKNSLYMVEYVAGGEMFSLHURIGRFAEPHARFYAAQI 143
QY 144 ASAGYLHSLNIYRDLPENILDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPEYLAP 203
Db 144 VLTFEYLHSLDIYRDLPENILDCQGVYQVTDGFAK--RVKGRWTWLCGTPEYLAP 200
QY 204 EVLRKEPYDRAVDWCLGAVLYEMHLGLPPFYSQDSQMYENILHQLPQIPGGRVAACD 263
Db 201 EILSKGYNKAVDMMWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFPFHSDDLKD 260
QY 264 LLOSLHKKDQORLGS-KADFLKHNHVFSPINWDDLHYKRLTPFPNPNVVTGPADLKH 322
Db 261 LURNLLQVLTFRKGNLKGNDIKNHWFAITDIAIYQKVEAPFIPKFGPGDTSNF 320
QY 323 DPEFTQEAIVSKI 335
Db 321 D-DYEEIEIRVSI 332
RESULT 9
US-11-132-142-13
; Sequence 13, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:

; APPLICANT: The Burnham Institute
 ; APPLICANT: Sikora, Sergey
 ; APPLICANT: Godzik, Adam
 ; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
 ; FILE REFERENCE: 8014-011-US
 ; CURRENT APPLICATION NUMBER: US/11/132,142
 ; CURRENT FILING DATE: 2005-05-17
 ; PRIOR APPLICATION NUMBER: 60/571,698
 ; PRIOR FILING DATE: 2004-05-17
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 13
 ; LENGTH: 351
 ; TYPE: PRT
 ; ORGANISM: Xenopus sp.
 US-11-132-142-13

Query Match 35.5%; Score 694.5; DB 7; Length 351;
 Best Local Similarity 43.1%; Pred. No. 2.7e-56;
 Matches 135; Conservative 65; Mismatches 106; Indels 7; Gaps 5;

Qy	24	PSANPNAQPTDFDLVKVKGNYGKVLAKRSDGAFYAVKVLQKKSILKKKEQSHIAE	83
Db	34	PPQN-TASLDPDFRDKTLTGTSFGKVMVLVKHGAQYYAMKILDKQKVVKLQKQIETLNE	92
Qy	84	RSVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGELFFHLQRRRRFLEPRARYAAEV	143
Db	93	KRI-LQAVNFFFLVRLEYSFKDNSNLYIMEVPGSEMFSLRRIGRSEPHARYAAQI	151
Qy	144	ASATGYLHSLNIYRDLPENILDCQGHVLTDFGLCKEGVEPDDTSTFCGTPEYLAP	203
Db	152	VLTFEYLSLSDLIYRDLPENLLIDQOQYIQVTDGFAK--RVKGRVTWLCGTPEYLAP	208
Qy	204	EVLKPEPYDRAVDNWCGLGAVLYEMLHGLPPYVSQDSOMVENILHQPQLICGRITVAACD	263
Db	209	EILSKGVKAVDANWALGVLIYEWAAGYPPFFAQDQIYIKIVSGKVRFPFHSDDLKD	268
Qy	264	LLOSLHKKDQRQLGS-KADFEIKNHVFFSPINWDDLYHKRLTPFPNPNVTGPADLKH	322
Db	269	LLRNLQVLDLTKRYGNLKNGVNDIKNKKWFATTDWIAIYQKVEAPFIPKCGPGDTSNF	328
Qy	323	DPEFTQEAIVSKI	335
Db	329	D-DYEEEDIRVSL	340

RESULT 10
 US-11-132-142-14
 ; Sequence 14, Application US/11132142
 ; Publication No. US20050276818A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Burnham Institute
 ; APPLICANT: Sikora, Sergey
 ; APPLICANT: Godzik, Adam
 ; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
 ; FILE REFERENCE: 8014-011-US
 ; CURRENT APPLICATION NUMBER: US/11/132,142
 ; CURRENT FILING DATE: 2005-05-17
 ; PRIOR APPLICATION NUMBER: 60/571,698
 ; PRIOR FILING DATE: 2004-05-17
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 14
 ; LENGTH: 351
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-132-142-14

Query Match 35.4%; Score 691.5; DB 7; Length 351;
 Best Local Similarity 43.1%; Pred. No. 5.1e-56;
 Matches 135; Conservative 65; Mismatches 106; Indels 7; Gaps 5;

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QY 323 DPEFTQEA 331
Db 440 D-EYEEAL 447

RESULT 12
US-10-497-767-4
; Sequence 4, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOVORKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VPI/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497,767
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (338)
; OTHER INFORMATION: Variable amino acid
US-10-497-767-4

Query Match 34.9%; Score 681.5; DB 6; Length 350;
Best Local Similarity 42.5%; Pred. No. 4.2e-55;
Matches 133; Conservative 65; Mismatches 108; Indels 7; Gaps 5;

QY 24 PSANPAQPTDFDLKVGKNGYKVLAKRSDGAFYAVKVLQKKSILKKKEQSHIMAE 83
Db 33 PAQN-TAHLDDQFERIKLTGTSGSRVWLKHMETGNHYAMKILDKQVKVQLQIEHTLNE 91

QY 84 RSVLLKNVRHPFLVGURYSGFQTEPKLYFVLDYVNGGELFFHLQRRRFLPRARFYAAEV 143
Db 92 KRI-LQAVNFPFLVKLEFSKONSILYMWMEYVPGGEMFSLRRIGRFSEPHARFYAAQI 150

QY 144 ASAIGYLHSLNIYRDLKPENLILDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPEYLAP 203
Db 151 VLTFEYLHSLDLIYRDLKPENLILDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPEYLAP 207

QY 204 EVLRKEPYDRADVWCLGAVLYEMLHGLPPYSQDVSMYENILHQLPIPGGRTVAACD 263
Db 208 EILSGYKXAVDWALGVLIYEMAGYPPFPADQPIQYKIVSKVRFPFHSDDLKD 267

QY 264 LIQSLHDKQORLGS-KADFLKHNHVFSPINWDDLYHKRLTPFPNPNVTGPADLKH 322
Db 268 LLRNLLQVLDLTKRFGNLKGVNDIKNKKWFATTDIAIYQKVEAFPIPKFGPGDTSNF 327

QY 323 DPEFTQEA 335
Db 328 D-DYEEERIVXI 339

RESULT 13
US-11-132-142-9
; Sequence 9, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
```

```
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 9
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Leishmania sp.
US-11-132-142-9

Query Match 34.9%; Score 681.5; DB 7; Length 381;
Best Local Similarity 42.0%; Pred. No. 4.7e-55;
Matches 136; Conservative 62; Mismatches 113; Indels 13; Gaps 5;

QY 33 TDDFELKVGKNGYKVLAKRSDGAFYAVKVLQKKSILKKKEQSHIMAEKRSVLLKNVR 92
Db 70 SDFELKNTLGTSGFRVIAHRKGTGEYYAIKLRKREIIRKMQQOHVAQEGILME-LC 128

QY 93 HPFLVGLRYSFOTPEKLYFVLDYVNGGELFFHLQRRRFLPRARFYAAEVAASIGYLHS 152
Db 129 HPFIYMMCMSPDEKKVIFLLEFVNGGEMFTHLRTAGFPNDVAFYHAEVLVAPEYLHS 188

QY 153 LNIYRDLKPENLILDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPEYLAPVLRKPYD 212
Db 189 LDVIYRDLKPENLILDNKGHVKTDFGPAK---KVPDRTFTLCGTPEYLAPVLSQKHG 245

QY 213 RAVDWCLGAVLYEMLHGLPPYSQDVSMYENILHQLPIPGGRTVAACDLQSLHDK 272
Db 246 KAVDWMTMGVLLYEFYAGYPPFDTPPRIYEKILAGRLKFPNWFGRARDLVKGLLQTD 305

QY 273 QRORLGS-KADFLKHNHVFSPINWDDLYHKRLTPFPNPNVTGPADLKHDFPEFTQEA 331
Db 306 HTKRLGTUUGPADVKNHPYFHGANWDLKLYARYYPAPVPRVKSFGDTSNFE-KYPDSPV 364

QY 332 SKSIGCTPDTVASSSGASSAFLGF 355
Db 365 DR-----TPALTSAQQAELKGF 381

RESULT 14
US-10-995-561-856
; Sequence 856, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 856
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-856

Query Match 34.9%; Score 681; DB 6; Length 705;
Best Local Similarity 39.8%; Pred. No. 1.2e-54;
Matches 139; Conservative 60; Mismatches 138; Indels 12; Gaps 3;

QY 9 PSPQPSRANGNINLQPSANPNAQPTDFDLKVGKNGYKVLAKRSDGAFYAVKVLQK 68
Db 359 PEPELNKER-----PSLQIKLKIEDFILHMKLGKSGFKVFLABFKKTKNQFPAIKALKK 412
```

QY 69 KSLKKKQSHMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGELFFHLQRE 128
Db 413 DVVLMDDDDVECTWVEKRVLSLAWEHFLLTHMFTCTQTKENLFFVMEYINGGDLMYHIQSC 472
QY 129 RRFLEPRARFYAAEVAASAIYGLHSLNIIYRDLPENILLDCQGHVLTDFGLCKEGVEPE 188
Db 473 HKFDLSRATFYAAEIIQLGLFHSKGIVYRDLLKDNILLDKDGHIKIADFGMCKENMLGD 532
QY 189 DTTSTFCGTPYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVSQMYENILH 248
Db 533 AKTNTFCGTPDYIAPEILLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEELFHSIRM 592
QY 249 QPLQIFGGRTVAAACDLLOSLHKKQORIGSKADFLFIKNHVFPSPINWDDLYHKRLTTP 308
Db 593 DNPFFYRWLEKEAKOLLVLFVREPEKRLGVRGD---IRQHPLEINWEELEERKEIDPP 649
QY 309 FNPNTGPDADLKHFDPEFTQEAHSVSKSIGCTPDTVASSSGASSAFLGFSY 357
Db 650 FRPKVSPFDCSNFDEFLNEKPRLSFA---DRALINSMQDNMFRNFSF 695

RESULT 15

US-10-995-561-855
; Sequence 855, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 855
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-855

Query Match 34.9%; Score 681; DB 6; Length 706;
Best Local Similarity 39.8%; Pred. No. 1.2e-54;
Matches 139; Conservative 60; Mismatches 138; Indels 12; Gaps 3;

QY 9 PSPQPSRANGNINIGPSANPNQPTDFLKVIGKNGYKVLAKKSDGAFYAVKVLQK 68
Db 360 PEPENKER-----PSLQIKLKIEDFILHKMLGSGFGKVLAEFPKTNQFPAIKALKK 413
QY 69 KSLKKKQSHMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGELFFHLQRE 128
Db 414 DVVLMDDDDVECTWVEKRVLSLAWEHFLLTHMFTCTQTKENLFFVMEYINGGDLMYHIQSC 473
QY 129 RRFLEPRARFYAAEVAASAIYGLHSLNIIYRDLPENILLDCQGHVLTDFGLCKEGVEPE 188
Db 474 HKFDLSRATFYAAEIIQLGLFHSKGIVYRDLLKDNILLDKDGHIKIADFGMCKENMLGD 533
QY 189 DTTSTFCGTPYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVSQMYENILH 248
Db 534 AKTNTFCGTPDYIAPEILLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEELFHSIRM 593
QY 249 QPLQIFGGRTVAAACDLLOSLHKKQORIGSKADFLFIKNHVFPSPINWDDLYHKRLTTP 308
Db 594 DNPFFYRWLEKEAKOLLVLFVREPEKRLGVRGD---IRQHPLEINWEELEERKEIDPP 650
QY 309 FNPNTGPDADLKHFDPEFTQEAHSVSKSIGCTPDTVASSSGASSAFLGFSY 357
Db 651 FRPKVSPFDCSNFDEFLNEKPRLSFA---DRALINSMQDNMFRNFSF 696

Search completed: January 27, 2006, 23:58:23
Job time : 11.4635 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:12:00 ; Search time 10.8484 Seconds
(without alignments)
3254.993 Million cell updates/sec

Title: US-09-868-131a-1

Perfect score: 1954
Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFLGFSYAPEDDDILDC 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1413	72.3	431	2 A48094	serum and glucocor
2	983	50.3	422	2 T23334	hypothetical prote
3	886	45.3	479	1 A53980	protein kinase (EC
4	878.5	45.0	462	1 T17287	protein kinase (EC
5	878.5	45.0	480	1 S33364	protein kinase (EC
6	878.5	45.0	763	1 A40831	gag-akt polyprotel
7	877.5	44.9	454	1 JC4345	protein kinase (EC
8	876	44.8	481	1 A48288	protein kinase (EC
9	875.5	44.8	480	1 JC2437	protein kinase (EC
10	874.5	44.8	480	1 A39360	protein kinase (EC
11	866	44.3	680	2 S37955	protein kinase YPK
12	863.5	44.2	480	1 S62117	protein kinase (EC
13	862	44.1	481	1 JC2438	protein kinase (EC
14	852	43.6	479	2 A38578	protein kinase 2 (
15	846	43.3	677	2 JS0178	protein kinase YKR
16	835.5	42.8	611	1 A53888	protein kinase (EC
17	803	41.1	569	2 T50414	probable prolifera
18	791	40.5	586	2 A53758	protein kinase C (
19	791	40.5	587	2 A49509	protein kinase C (
20	789.5	40.4	646	2 T38171	probable serine/ch
21	789	40.4	481	2 JE0377	p70 S6 kinase (EC
22	788	40.3	546	1 T43233	protein kinase (EC
23	787	40.3	1016	1 A46079	protein kinase C (
24	783.5	40.1	541	1 T43232	protein kinase (EC
25	778	39.8	525	1 A41687	ribosomal protein
26	778	39.8	525	1 S12906	probable ribosomal
27	776	39.7	634	1 B32392	protein kinase C (
28	769.5	39.4	696	2 S55694	protein kinase (EC
29	769	39.4	525	1 TVRTK6	ribosomal protein

RESULT 1

A48094

serum and glucocorticoid-regulated kinase - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004

C:Accession: A48094

R:Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.

Mol. Cell. Biol. 13, 2031-2040, 1993

A:Title: Characterization of sgk, a novel member of the serine/threonine protein kinase

A:Reference number: A48094; MUID:93204949; PMID:8455596

A:Accession: A48094

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-431 <WEB>

A:Cross-references: UNIPARC:UPI000017AJE8

A:Experimental source: Con8.hd6 mammary epithelial tumor cells

A>Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBIPI:127619)

C:Keywords: ATP

F:96-355/Domain: protein kinase homology <KIN>

F:104-112/Region: protein kinase ATP-binding motif

Query Match	72.3%	Score	1413;	DB	2;	Length	431;
Best Local Similarity	70.9%	Pred. No.	8.5e-60;				
Matches	261;	Conservative	56;	Mismatches	43;	Indels	8;
Gaps	3;						
QY	1	MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFDKVIGKNGYKVVLLAKRKSDGAF	60				
Db	69	MNANP--SPPPSPSQ---QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEAF	123				
QY	61	YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPFLVGLRYSPQTEPKLYFVLVDYVNGGE	120				
Db	124	YAVKVLQKKAALKKKEKHIMSERNVLLKNVRHPFLVGLHFSQFADKLYFVLVDYINGGE	183				
QY	121	LFPHLQRRERFLPRARFYAAEVAISAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL	180				
Db	184	LFPHLQRRERFLPRARFYAAEVAISAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL	243				
QY	181	CKGEVEPDDTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPPFYSDVS	240				
Db	244	CKENIEHNGTSTFCGTPPEYLAPEVLKPEYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA	303				
QY	241	QYENILHQPLOIPGGRVTVAACDLQSLHKKDOROLSKADPLETKNHVFPSPINWDDL	300				
Db	304	EMYDNLNKLPLQKNTINSARHLEGLQKDKRTKRLGAKDDFMETKSHIFPSLINWDDL	363				
QY	301	YHKRLTPFPNPNVTGPADLKHPDPEFTQEAWSKSGCTPDTV---ASSSGASSAFLGFSY	357				
Db	364	INKKLTTPFPNPNVSGPSDLRHPDPEFTPEVPSSIGRSPDSILVTASVKEAAEFLGFSY	423				
QY	358	APEDDDIL 365					
Db	424	APPMDSFL 431					

protein kinase C (JN0877
protein kinase C (A30314
protein kinase C (JCI480
protein kinase C (KIMSCE
protein kinase C (S28942
protein kinase C (KIRBCE
protein kinase C (T43051
hypothetical prote
protein kinase C (S61917
protein kinase C (T21523
protein kinase C (A53530
protein kinase C (KIBOGC
protein kinase C (S29478
protein kinase C (A23690
ribosomal protein I51901

RESULT 2

T26334

hypothetical protein W10G6.2 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004

C:Accession: T26334

R:McMurray, A.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z20201

A:Accession: T26334

A:Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: DNA

A:Residues: 1-422 <W1>

A:Cross-references: UNIPROT:Q94365; UNIPARC:UPI000007852E; EMBL:Z81140; PIDN:CAB03485.1

A:Experimental source: clone W10G6

C:Genetics:

A:Gene: CESP:W10G6.2

A:Map position: X

A:Introns: 14/3; 60/2; 88/2; 135/3; 179/3; 217/2; 290/3; 393/1

Query Match 50.3%; Score 983; DB 2; Length 422;

Best Local Similarity 54.7%; Pred. No. 1.2e-39;

Matches 176; Conservative 57; Mismatches 89; Indels 0; Gaps 0;

Qy 13 PSRANGNINLPSANPNAAQPTDFELFKVIGKNGYKVLAKRKSDGAFYAVKVLQKKSIL 72

Db 72 PDDDENNDLGPSEKTKATANDFDYLTIGKSGFRVYQVRHKETKKIYANKILSKEHIR 131

Qy 73 KKEEQSHIMAEKRSVLLKNVRHPIVLGRYSGFTPEKLYFVLVDYVNGGELFFHLQRRRFL 132

Db 132 KQNEVKHMAERNVLINFNKHPFLVLSHFSGFNQKELKLYFVLVDHLNGGELFSHLQREKHS 191

Qy 133 EPRARFYAAEVAASAIQVLSHNSIITYRDLKPENLILDCQGHVLTDFGLCKEGVEPEPTTS 192

Db 192 ESKSRFYAAETACALGYLHEKNIITYRDLKPENLILDCQGHVLTDFGLCKEDMQGSKTTS 251

Qy 193 TFCGTPPYLAPEVLKPEPYDRAVDWVCLGAVLYEMLHGLPPFYSDQVSQVYENILHQPLO 252

Db 252 TFCGTPPYLAPEIILKKPYDKTVDWVCLGSLVYEMISGLPPFYSKDHNEMVDKLIINQPLR 311

Qy 253 IPGGRTVAACDLQSLGHLKQORQLGSKADFLEIKNHVFFSPINWDDLYHKRLTPPPFPNP 312

Db 312 LKHNISVPCSELITGLLKQKRSKGLHRNDFRDIRDHPFELPVDWDKLLNRELKAPPFKP 371

Qy 313 VTGPGADLKHPDPEFTQEAWSKS 334

Db 372 VKNAMDTSNISKEFVEIQIDPS 393

RESULT 3

A59380

protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human

N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protease

C:Species: *Homo sapiens* (man)

C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004

C:Accession: A59380; A59379

R:Brodebeck, D.; Cron, P.; Hemmings, B.A.

J. Biol. Chem. 274, 9133-9136, 1999

A:Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the activation

A:Reference number: A59380; MUID:99194749; PMID:10092583

A:Accession: A59380

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-479 <BRO>

A:Cross-references: UNIPROT:Q9Y243; UNIPARC:UPI00000335E8; GB:AAD29089; NID:Q4757579; PI

R:Masure, S.; Haefner, B.; Wesselink, J.J.; Hoefnagel, E.; Mortier, E.; Verhaesselt, P.;

Eur. J. Biochem. 265, 353-360, 1999

A:Title: Molecular cloning, expression and characterization of the human serine/threonin

A:Reference number: A59379; MUID:99421751; PMID:10491192

A:Accession: A59379

A:Status: preliminary

A,Molecule type: DNA
A;Residues: 1-479 <MAS>
A;Cross-references: UNIPARC:UPI0000335B8; GB:CAB53537; NID:g5804886; PIDN:CAB53537.1
C;Genetics:
A;Gene: GDB:AKT3; PKBG: PRKBG; RAC-gamma
A;Cross-references: GDB:9954867
A;Map position: lq44-lq44
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein C;
Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F;7-108/Domain: pleckstrin repeat homology <PLK>
F;149-408/Domain: protein kinase homology <KIN>
F;157-165/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted
F;305/Binding site: phosphate (Thr) (covalent) #status predicted
F;474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 45.3%; Score 886; DB 1; Length 479;
Best Local Similarity 48.4%; Pred. No. 4.7e-35;
Matches 181; Conservative 55; Mismatches 100; Indels 38; Gaps 8;

QY 1 MNSSPAGTSPDPSRAN--GNINLGPSANPNQAQT--DFDFLKVIQKGNGVKVLLAKRKS 56
|| || | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 117 MNCSP-----SQINDIGESMDASTTHHKRKTMNDFDYLKLCKGTFGKVILVREKA 169

QY 57 DGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPELVGLGRYSFTQPEKLYFVLVDYV 116
|| || | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 170 SGKGYAMKLIKKEVIIIAKDEVAHTTE-SRVLKNTRHPFLTSLKYISFOFKDLCLCFVMXYV 228

QY 117 NGGELEFHQLQRERRFLPRARFYAAEVSAAIGVLSLNIIYRDLPENILLDCQGHVILT 176
|| || | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 229 NGGELEFHLRSRRVSESDRTRYGAEIVSALDYLSHGKIYYRDLKLENLMLDKGHIKIT 288

QY 177 DFGLCKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDVADVWMCGLGAVLYEMLHGLPPFPY 236
|| || | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 289 DFGLCKEGITDAATMTKTCGTPEYLAPEVLEDNDYGRAVDWNLGLGVVMYMMCGRLPFYN 348

QY 237 QDVSYQMYENILHQPLQIPGRVTACVADLLQSLLHKDQORL-GSKADFLEIKNVFFSF 295
|| || | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 349 QDEHKLFEILIMEDIKFPRTLSSDKASLLSGLLI KDPNKRLGGPGDDAKEIMRHGSFFSGV 408

QY 296 NWDDLHYKELTPFNPNVTVGPADLKHDFDEFTOEAVSKSIGCTPDTVASSSGASSAFILGF 355
|| || | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 409 NWQDVVDKLVLPFPKPQVTSFTDTRYDFDEFT----AQITITP----- 448

QY 356 SYAPE---DDDILDC 367
|| || | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 449 ---PEKYDEGDGWC 459

RESULT 4
TI7287
protein kinase (EC 2.7.1.37) akt3 short splice form - human
N;Alternate names: protein kinase B gamma; RAC-PK-gamma, serine/threonine-specific protei
C;Species: Homo sapiens (man)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C;Accession: TI7287
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18723
A;Accession: TI7287
A:Molecule type: mRNA
A;Residues: 1-462 <POU>
A;Cross-references: UNIPARC:UPI000016ACT77; EMBL:AL117525; GB:CAB55977; NID:g5912043; PFI
A;Experimental source: adult testis; clone DKZzp434NO250
R;Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.; Roth, R.
J. Biol. Chem. 274, 21528-21532, 1999
A;Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and andrpg9
A;Reference number: A64199; PMID:10419456
A;Comments: This protein is increased in estrogen receptor-negative breast cancers and ar
C;Comments: annotation

C:Genetics:
A:Gene: GDB:AKT3
A:Cross-references: GDB:9954867
A:Map position: 1q44-1q44
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F:4-105/Domain: pleckstrin repeat homology <PLK>
F:146-405/Domain: protein kinase homology <KIN>
F:154-162/Region: protein kinase ATP-binding motif
F:177/Active site: Lys #status predicted

Query Match 45.0%; Score 878.5; DB 1; Length 462;
Best Local Similarity 51.0%; Pred. No. 1e-34;
Matches 172; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

QY 1 MNSSPAGTSPQSRAN--GNINLSPSANPNAQPT--DFDFLKVIKGNVGVKLLAKRKS 56
Db 117 MNCSP-----SQIDNIGEEMDASTTHHKRKTWDFYLLKLGKTFGKVLVREKA 169

QY 57 DGAFYAVKVLQKKSILKKKEQHMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDVY 116
Db 170 SGKYYAMKILKKKEVIAKDEVAHTLTS-SRVLNTRHPLFTSLKYSFQTKDLRCFYMEYV 228

QY 117 NGGELFHLQRERREPRARFYAAEVAASVAGVLSNLIYRDLKPNILLDCQGHVILT 176
Db 229 NGGELFHLQRERREPRARFYAAEVAASVAGVLSNLIYRDLKPNILLDCQGHVILT 176

QY 177 DFGLCKEGVEPDTTSTFCGTPPEYLAPVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFY 236
Db 289 DFGLCKEGITDAATMTKTCGTPPEYLAPVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFY 348

QY 237 QDVQMYENILHQPQIPEGRTVAACDLQSLHKKQORL-GSKADFLKINHNVPFSP 295
Db 349 QDHEKLFELIMEDIKFPRTLSGKSLGLLKDQPNKRLGGGPDDAKEIMRHSFSGV 408

QY 296 NDDDLVHKLTPFPNPNVTPGADLKHDPDEFTQEAUS 332
Db 409 NQWQVDYDKLVPPFKQVTSSETDTRYDFEETQAQIT 445

RESULT 5
S33364
protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: S33364
R:Bellocosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner, J
Oncogene 8, 745-754, 1993
A:Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt a
A:Reference number: S33364; MUID:93173519; PMID:8437858
A:Accession: S33364
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-480 <BEL>
A:Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PID
C:Genetics:
A:Gene: MGI:Akt
A:Cross-references: MGI:87986
A:Map position: 12
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki

F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 45.0%; Score 878.5; DB 1; Length 480;
Best Local Similarity 47.8%; Pred. No. 1.1e-34;
Matches 175; Conservative 58; Mismatches 102; Indels 31; Gaps 7;

QY 6 ACTPSPQPSRANGNINLSPSANPNAQPT--DFDFLKVIKGNVGVKLLAKRKSDFGAFYAV 63
Db 122 SGSPSDNSCAEEMVSL---AKPKHRTVWNEFEYLKLGKTFGKVLVKEKATGRYAM 178

QY 64 KVLQKKSILKKKEQHMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDVYNGELPFF 123
Db 179 KILKKEVIVAKDEVAHTLTENRV-LQNSRHPLTALKYSFQTHDRLCFVMEYANGELPFF 237

QY 124 HLQRERRRLEPRARFYAAEVAASVAGVLSNLIYRDLKPNILLDCQGHVILTDFGLCK 182
Db 238 HLQRERRRLEPRARFYAAEVAASVAGVLSNLIYRDLKPNILLDCQGHVILTDFGLCK 297

QY 183 EGVEPEPDTTSTFCGTPPEYLAPVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVSQM 242
Db 298 EGKDGATMKTTCGTPPEYLAPVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVSQM 357

QY 243 YENILHQPQIPEGRTVAACDLQSLHKKQORL-GSKADFLKINHNVPFSPINWDDLY 301
Db 358 FELIIMEEIRPRTLGPPEAKSLGLLKKDPTQRLGGGSEDAKEIMQHRFFANIVMQDVY 417

QY 302 HKRLTPFPNPNVTPGADLKHDPDEFTQEAUSKISGCTPTTVASSSSGASAFGLFSVAPED 361
Db 418 EKLSPPFPKQVTSSETDTRYDFEETQAQIT----ITP-----PDQ 454

QY 362 DDILDC 367
Db 455 DDMSEC 460

RESULT 6
A40831
gag-akt polyprotein - AKT8 murine leukemia virus
N:Contains: amino end of core protein p30; core protein p15; inner coat protein p12; k1.
C:Species: AKT8 murine leukemia virus
C:Date: 12-Feb-1993 #sequence_revision 12-May-1994 #text_change 31-Dec-2004
C:Accession: A40831; B40831
R:Bellocosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.
Science 254, 274-277, 1991
A:Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an S
A:Reference number: A40831; MUID:92022574; PMID:1833819
A:Accession: A40831
A:Molecule type: DNA
A:Residues: 1-262 <BEL>
A:Cross-references: UNIPARC:UPI000001725AF; GB:M80675
A:Accession: B40831
A:Molecule type: DNA
A:Residues: 262-763 <BE2>
A:Cross-references: UNIPARC:UPI000001725B0; GB:M80675
C:Genetics:
A:Gene: gag-akt
C:Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransfera
F:1329/Product: core protein p15 #status predicted <CP1>
F:130-214/Product: inner coat protein p12 #status predicted <CP2>
F:284-763/Product: kinase-related transforming protein akt #status predicted <AKT>
F:287-389/Domain: pleckstrin repeat homology <PLK>
F:431-691/Domain: protein kinase homology <KIN>
F:439-447/Region: protein kinase ATP-binding motif
F:25,337/Binding site: carboxylate (Asn) (covalent) #status predicted
F:462/Active site: Lys #status predicted
F:609/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 45.0%; Score 878.5; DB 1; Length 763;
Best Local Similarity 47.8%; Pred. No. 1.6e-34;
Matches 175; Conservative 58; Mismatches 102; Indels 31; Gaps 7;

QY 6 ACTPSPQPSRANGNINLSPSANPNAQPT--DFDFLKVIKGNVGVKLLAKRKSDFGAFYAV 63
Db 122 SGSPSDNSCAEEMVSL---AKPKHRTVWNEFEYLKLGKTFGKVLVKEKATGRYAM 178

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Db 405 SGSPSDNSGAEEVMSL---AKPKHRTVMNEPEYLKLLGKGTGKVLVKEKATGRYYAM 461
QY 64 KVLQKSLKKKEQSHMAERSVLLKNVRHPPFLVGLRYSFOTPEKLYFVLVDYVNGGELEFF 123
Db 462 KILKKEVIVAKDEVAHTLTENRV-LQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELEFF 520
QY 124 HLQRRRFLPEPRARFYAAAEVASAIGVLHS-LNIYRDLKPENILLDCQGHVLTDFGLCK 182
Db 521 HLSRERVFSEDRARFYGAIVSALDYLHSEKNVVYRDLKLENMLDKDGHIKITDFGLCK 580
QY 183 EGVEPEDTTSFGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDVSQM 242
Db 581 EGIKGATMKTFCGTPEYLAPEVLEDNDYGRAVDMWGLGVVMYMMCGRLPFYNQDHEKL 640
QY 243 YENILHQIPIGGRVVAACDLLOSLLHKDQORQL-GSKADFLFIKKNHVFSPINWDDLY 301
Db 641 FELILMEERFRPRTLGPESAKSLLSGLLKDPQTRLGGSEDAKEIMQHRFFANIMQDYY 700
QY 302 HKRLTPFPNPNVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSVPED 361
Db 701 EKKLSPPFPQVTSSETDTRYFDEEFTAQMIT-----ITP-----PDQ 737
QY 362 DDILDC 367
Db 738 DDSMEC 743

RESULT 7
JC4345
protein kinase (EC 2.7.1.37) akt3 [validated] - rat
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: JC4345
R:Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K
Biochem. Biophys. Res. Commun. 216, 526-534, 1995
A:Title: Molecular cloning and characterization of a new member of the RAC protein kinase
e C subspecies and beta gamma subunits of G proteins.
A:Reference number: JC4345; MUID:96063640; PMID:7488143
A:Accession: JC4345
A:Molecule type: mRNA
A:Residues: 1-454 <KON>
A:Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DDBJ:D49836; NID:g1136777; PI
A:Experimental source: brain
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F:4-105/Domain: pleckstrin repeat homology <PLK>
F:146-405/Domain: protein kinase homology <KIN>
F:154-162/Region: protein kinase ATP-binding motif
F:177/Active site: Lys #status predicted

Query Match 44.9%; Score 877.5; DB 1; Length 454;
Best Local Similarity 51.0%; Pred. No. 1.1e-34;
Matches 172; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

QY 1 MNSSPAGTSPSPSRAN--GNINLGFSANPNQAQT--DFDFLKVIKGNKYGVLLAKRKS 56
Db 117 MNCSP-----SQIDNIGEEEMDASTTHHKRTMWNDFYLLKLGKTFGKVLVREKA 169
QY 57 DGAFYAVKVLQKSLKKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTEKLYFVLVDY 116
Db 170 SGKYYAMKLLKKEVITAKDEVAHTLTS-SRVLKNTRHPFLTSLKYSFQTKDRLCFVMEYV 228
QY 117 NGSELFFHLQRRRRFLPEPRARFYAAAEVASAIGVLHSLNIIYRDLKPENILLDCQGHVLT 176
Db 229 NGSELFFHLSRERVFSEDRTRYGAIVSALDYLHSGKVIYRDLKLENMLDKDGHIKIT 288
QY 177 DFGLCKEGVEPEDTTSFGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFY 236
Db 289 DFGLCKEGITDAATMKTFCGTPEYLAPEVLEDNDYGRAVDMWGLGVVMYMMCGRLPFYN 348
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QY 237 ODVSQMYENILHQIPIGGRVVAACDLLOSLLHKDQORLGSKADP-LEIKNHVFFSP 295
Db 349 QDHEKLFELIMEDIKFPRTLUSSDAKSLLSGLLIKIDPNKRLGGGPDPKBEIMRHSFFSGV 408
QY 296 NMDDILYHKRLTPFPNPNVTGPADLKHFDPEFTQEAHSV 332
Db 409 NWQDYYDKLVPFPFQVTSSETDTRYFDEEFTAQMIT 445
```

RESULT 8

```
A46288
protein kinase (EC 2.7.1.37) akt2 - human
N:Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protei
C:Species: Homo sapiens (man)
C:Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
C:Accession: A46288
R:Cheng, J.O.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; :
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992
A:Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/th
A:Reference number: A46288; MUID:93028445; PMID:1409633
A:Accession: A46288
A:Molecule type: mRNA
A:Residues: 1-481 <CHE>
A:Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M95936; NID:g178325; PIDN
A:Note: sequence extracted from NCBI backbone (NCBIP:115859)
C:Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.
C:Genetics:
A:Gene: GDB:AKT2
A:Cross-references: GDB:135660; OMIM:164731
A:Map position: 19q13.2-19q13.2
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:150-409/Domain: protein kinase homology <KIN>
F:158-166/Region: protein kinase ATP-binding motif
F:181/Active site: Lys #status predicted
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```
Query Match 44.8%; Score 876; DB 1; Length 481;
Best Local Similarity 48.9%; Pred. No. 1.4e-34;
Matches 174; Conservative 57; Mismatches 113; Indels 12; Gaps 5;
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QY 10 SPQSPRANGNINLGFS-ANPNQAQTFDFFLKVIKGNKYGVLLAKRKS DGAFYAVKVLQK 68
Db 126 SPDSSTTEMEVAVSKARAKVTMWNDFYLLKLGKTFGKVLVREKATGRYYAMKILRK 185
QY 69 KSILKKKQSHMAERSVLLKNVRHPPFLVGLRYSFQTEKLYFVLVDYVNGGELFHLQRE 128
Db 186 EVIIAKDEVAHTVTS-SRVLQNTRHPPFLTALKYAFQTHDRLCFVMEYANGGELFHLRSR 244
QY 129 RFLPEPRARFYAAAEVASAIGVLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKEGVEPE 188
Db 245 RVFTTEARFYGAIEIVSALEYLHSDVDVYRDLKLENMLDKDGHIKITDFGLCKEGISDG 304
QY 189 DTTSTFCGTPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFYSDVSQMYENILH 248
Db 305 ATMTKTCGTPEYLAPEVLEDNDYGRAVDMWGLGVVMYEMMCGRLPFYNQDHERL FELILM 364
QY 249 QPLQIPGGRVVAACDLLOSLLHKDQORQL-GSKADFLFIKKNHVFSPINWDDLYHKRLTP 307
Db 365 EEIRFPRTLSPKASLLAGLLKKDQKRLGGGSDAKEMVMEHRFSLSNWQDVQVKLLP 424
QY 308 PNPNPVTGPADLKHFDPEFTQEAHSVKSIGCTPDTVASSSG-----ASSAFLGFSYA 358
Db 425 FPKQVTSVDTTRYFDDEFT-----AQSTITTPDRYDLSGLLELDQRTHPQFSYS 476
```

RESULT 9

```
JC2437
protein kinase (EC 2.7.1.37) akt1 [validated] - rat
```

R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A;Reference number: S24423; MUID:92249329; PMID:1533586
A;Contents: erratum
A;Accession: S36389
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477,
A;Cross-references: UNIPARC:UPI000016AEB1; EMBL:X61037; NID:g35480; PIDN:CAA43372.1; PI:1
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991
A;Note: this a revision to the sequence from reference S17999
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kina
A;Reference number: S17999; MUID:92037600; PMID:1718748
A;Accession: S18000
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 63-70, 'TPSSAACSGPLSNAPSMWLLRSGGVNDRHPDCRRPQ', 'EAGGGDGLPVGLTORQLRGRDRGG
A;Cross-references: UNIPARC:UPI00001725AB; EMBL:X61037
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
A;Note: this sequence has been revised in reference S24423
R;Coffer, P.
submitted to the EMBL Data Library, July 1991
A;Reference number: S20836
A;Accession: S20836
A;Molecule type: mRNA
A;Residues: 63-70, 'TPSSAACSGPLSNAPSMWLLRSGGVNDRHPDCRRPQ', 'EAGGGDGLPVGLTORQLRGRDRGG
A;Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037
A;Note: this sequence has been revised in reference S24423
R;Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemmin
EMBO J. 15, 6541-6551, 1996
A;Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
A;Reference number: A64192; MUID:97133284; PMID:8978681
A;Contents: annotation; phosphorylation sites
R;Toker, A.; Newton, A.C.
J. Biol. Chem. 275, 8271-8274, 2000
A;Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical p
A;Reference number: A64193; MUID:20187529; PMID:10722653
A;Contents: annotation; autophosphorylation site
C;Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidyl-
nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.
C;Genetics:
A;Gene: GDB:AKT1; RAC; PKB
A;Cross-references: GDB:118989; OMIM:164730
A;Map position: 14q32.32-14q32.32
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
e production
A;Pathway: signal transduction pathways regulating various processes including insulin
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experim

Query Match 44.8%; Score 874.5; DB 1; Length 480;
Best Local Similarity 47.5%; Pred. No. 1.6e-34;
Matches 174; Conservative 59; Mismatches 102; Indels 31; Gaps 7;
QY 6 AGTPSPQPSRANGNINLGSANPNQAQT--DFDFLKVIQKGNVGVKLLAKRSDGAFYAV 63
DB 122 SGPSSDNGSAERMEVSL---AKPKHRTVTNNEFEYLKLGKFTGKVLVKEKATGRYAM 178
QY 64 KVLQKSLKKKEQSHMAERSVLLKGVNHPFLVGLRYSFOTPEKLYFVLVDYVNGGELEF 123
DB 179 KILKKEVIVAKDEVVAHTLTENRV-QNSRHPFTALKYSFQTHDRLCFVWVEVANGGELEF 237
QY 124 HLQERRRFLPEPRFYAAEVAASVAGLYLHS-LNIIYRDLPENILLDCQGHVVLDTFGLCK 182

	Query Match	Score	DB 1;	Length	DB 2;	DB 3;	DB 4;	DB 5;	DB 6;	DB 7;	DB 8;	DB 9;	DB 10;	DB 11;	DB 12;	DB 13;	DB 14;	DB 15;	DB 16;	DB 17;	DB 18;	DB 19;	DB 20;	DB 21;	DB 22;	DB 23;	DB 24;	DB 25;	DB 26;	DB 27;	DB 28;	DB 29;	DB 30;	DB 31;	DB 32;	DB 33;	DB 34;	DB 35;	DB 36;	DB 37;	DB 38;	DB 39;	DB 40;	DB 41;	DB 42;	DB 43;	DB 44;	DB 45;	DB 46;	DB 47;	DB 48;	DB 49;	DB 50;	DB 51;	DB 52;	DB 53;	DB 54;	DB 55;	DB 56;	DB 57;	DB 58;	DB 59;	DB 60;	DB 61;	DB 62;	DB 63;	DB 64;	DB 65;	DB 66;	DB 67;	DB 68;	DB 69;	DB 70;	DB 71;	DB 72;	DB 73;	DB 74;	DB 75;	DB 76;	DB 77;	DB 78;	DB 79;	DB 80;	DB 81;	DB 82;	DB 83;	DB 84;	DB 85;	DB 86;	DB 87;	DB 88;	DB 89;	DB 90;	DB 91;	DB 92;	DB 93;	DB 94;	DB 95;	DB 96;	DB 97;	DB 98;	DB 99;	DB 100;	DB 101;	DB 102;	DB 103;	DB 104;	DB 105;	DB 106;	DB 107;	DB 108;	DB 109;	DB 110;	DB 111;	DB 112;	DB 113;	DB 114;	DB 115;	DB 116;	DB 117;	DB 118;	DB 119;	DB 120;	DB 121;	DB 122;	DB 123;	DB 124;	DB 125;	DB 126;	DB 127;	DB 128;	DB 129;	DB 130;	DB 131;	DB 132;	DB 133;	DB 134;	DB 135;	DB 136;	DB 137;	DB 138;	DB 139;	DB 140;	DB 141;	DB 142;	DB 143;	DB 144;	DB 145;	DB 146;	DB 147;	DB 148;	DB 149;	DB 150;	DB 151;	DB 152;	DB 153;	DB 154;	DB 155;	DB 156;	DB 157;	DB 158;	DB 159;	DB 160;	DB 161;	DB 162;	DB 163;	DB 164;	DB 165;	DB 166;	DB 167;	DB 168;	DB 169;	DB 170;	DB 171;	DB 172;	DB 173;	DB 174;	DB 175;	DB 176;	DB 177;	DB 178;	DB 179;	DB 180;	DB 181;	DB 182;	DB 183;	DB 184;	DB 185;	DB 186;	DB 187;	DB 188;	DB 189;	DB 190;	DB 191;	DB 192;	DB 193;	DB 194;	DB 195;	DB 196;	DB 197;	DB 198;	DB 199;	DB 200;	DB 201;	DB 202;	DB 203;	DB 204;	DB 205;	DB 206;	DB 207;	DB 208;	DB 209;	DB 210;	DB 211;	DB 212;	DB 213;	DB 214;	DB 215;	DB 216;	DB 217;	DB 218;	DB 219;	DB 220;	DB 221;	DB 222;	DB 223;	DB 224;	DB 225;	DB 226;	DB 227;	DB 228;	DB 229;	DB 230;	DB 231;	DB 232;	DB 233;	DB 234;	DB 235;	DB 236;	DB 237;	DB 238;	DB 239;	DB 240;	DB 241;	DB 242;	DB 243;	DB 244;	DB 245;	DB 246;	DB 247;	DB 248;	DB 249;	DB 250;	DB 251;	DB 252;	DB 253;	DB 254;	DB 255;	DB 256;	DB 257;	DB 258;	DB 259;	DB 260;	DB 261;	DB 262;	DB 263;	DB 264;	DB 265;	DB 266;	DB 267;	DB 268;	DB 269;	DB 270;	DB 271;	DB 272;	DB 273;	DB 274;	DB 275;	DB 276;	DB 277;	DB 278;	DB 279;	DB 280;	DB 281;	DB 282;	DB 283;	DB 284;	DB 285;	DB 286;	DB 287;	DB 288;	DB 289;	DB 290;	DB 291;	DB 292;	DB 293;	DB 294;	DB 295;	DB 296;	DB 297;	DB 298;	DB 299;	DB 300;	DB 301;	DB 302;	DB 303;	DB 304;	DB 305;	DB 306;	DB 307;	DB 308;	DB 309;	DB 310;	DB 311;	DB 312;	DB 313;	DB 314;	DB 315;	DB 316;	DB 317;	DB 318;	DB 319;	DB 320;	DB 321;	DB 322;	DB 323;	DB 324;	DB 325;	DB 326;	DB 327;	DB 328;	DB 329;	DB 330;	DB 331;	DB 332;	DB 333;	DB 334;	DB 335;	DB 336;	DB 337;	DB 338;	DB 339;	DB 340;	DB 341;	DB 342;	DB 343;	DB 344;	DB 345;	DB 346;	DB 347;	DB 348;	DB 349;	DB 350;	DB 351;	DB 352;	DB 353;	DB 354;	DB 355;	DB 356;	DB 357;	DB 358;	DB 359;	DB 360;	DB 361;	DB 362;	DB 363;	DB 364;	DB 365;	DB 366;	DB 367;	DB 368;	DB 369;	DB 370;	DB 371;	DB 372;	DB 373;	DB 374;	DB 375;	DB 376;	DB 377;	DB 378;	DB 379;	DB 380;	DB 381;	DB 382;	DB 383;	DB 384;	DB 385;	DB 386;	DB 387;	DB 388;	DB 389;	DB 390;	DB 391;	DB 392;	DB 393;	DB 394;	DB 395;	DB 396;	DB 397;	DB 398;	DB 399;	DB 400;	DB 401;	DB 402;	DB 403;	DB 404;	DB 405;	DB 406;	DB 407;	DB 408;	DB 409;	DB 410;	DB 411;	DB 412;	DB 413;	DB 414;	DB 415;	DB 416;	DB 417;
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Db 238 HLSRERFVSDRARFYGAIEVSALDYHSEKNVYVRDLXLENMLDKXGHIKITDGLCK 297
QY 183 EGVEPEDTTSCTGTPYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLUPPYQSQVSQM 242
Db 298 EGIKDGTAKTKTGTGTPYLAPEVLENDYGRAVDMWGLGVWVYEMMCGRLPFYNQDHEKL 357
QY 243 YENILHQPLOIGCGRTVAACDLLOSLLHKDQORLG--GSKADFLFIKHHVFSPINWDDLY 301
Db 358 FELLIMEEIRFRTUGPEAKSLLSGLLKKDKPQRLGGGSEDAKEIMQHRFFAGIVWQHY 417
QY 302 HRLTTPFPNVTGTPADLKHDFPEFTQEAUVSKSIGCTPDVTVASSSGASSAFLGFSYAPED 361
Db 418 EKKLSPPFKPQVTSIEDTRYDFEETFAQMIT----ITP-----PDQ 454
QY 362 DILDLC 367
Db 455 DDSMEC 460
RESULT 11
protein kinase YPK1 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
S37955
N:Alternate names: protein YKL126w
C:Species: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 05-Oct-2004
C:Accession: S37955; A31248; S30903
R:Ramazani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37953
A:Accession: S37955
A:Molecule type: DNA
A:Residues: 1-680 <RAM>
A:Cross-references: UNIPROT:P12698; UNIPARC:UPI000013BDPE; EMBL:Z28126; PID
A:Experimental source: strain S288C
R:Maurer, R.A.
DNA 7, 469-474, 1988
A:Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein
A:Reference number: A31248; MUID:89090805; PMID:2850145
A:Accession: A31248
A:Molecule type: DNA
A:Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>
A:Cross-references: UNIPARC:UPI0000168D89; EMBL:M21307; NID:G172180; PIDN:AAA34880.1; PI
K:Chen, P.; Lee, K.S.; Levin, D.E.
Mol. Gen. Genet. 236, 443-447, 1993
A:Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell gr
A:Reference number: S30903; MUID:93173125; PMID:8437590
A:Accession: S30903
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>
A:Cross-references: UNIPARC:UPI000017A451
C:Genetics:
A:Gene: SGD:YPK1
A:Cross-references: SGD:S0001609; MIPS:YKL126w
A:Map position: 11L
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:148-602/Domain: protein kinase homology <KIN>
F:353-361/Region: protein kinase ATP-binding motif
F:470/Active site: Asp #status predicted
Query Match 44.3%; Score 866; DB 2; Length 680;
Best Local Similarity 51.5%; Pred. No. 5.5e-34;
Matches 177; Conservative 53; Mismatches 106; Indels 8; Gaps 5;
QY 15 RANGINLGPSANPNQAQPTDFDLKVIKGNKGKVLAKRSDGAFYAVKVLQKKSILKK 74
Db 327 KINISIDYPSRNKPLSIDDFLLKVIKGNKGKVMQVRKKDTQKYALKARKSYIVSK 386
QY 75 EQSHIMAERSVLLKNVRHPLVGLRYSFQTPPEKLYFVLVDYVNGGELFFHLQRRFLRP 134
Db 387 SEVTHTLAERTVLAR-VDCPFIVPLKFSQSPEKLYFVLAFINGGELFFVHLQKGRFDLS 445
QY 135 RARFYAAEVAISGYLHSLNIYRDLKPNILDCQGHVVLDTDFGLCKGEVPEDTTSTF 194

Db 446 RARFYATALLCALDNLHKLDDVYRDLKPENILLDYQGHIALCDFGLCKLNMKDDKTDTF 505
QY 195 CQTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYQSQVSQMYENILHQPLOIP 254
Db 506 CQTPEYLAPELLGLGYTKAVDWMWTLGVLLYEMLTGLPPYDDEVPKMYKKILQELVFP 565
QY 255 GGRVAAACDLLOSLLHKDQORLG--SKADFLFIKHHVFSPINWDDLYHKLRTLPFPNPNV 313
Db 566 DGDFDRAKDLGLLSRDPTRRLGYNGAD--EIRNHPFSQLSWKRLLMKGYIPYPKPAV 623
QY 314 TGPADLKHDFPEFTQEAUVSKSIGCTPDVTVASSSGASSAFLGFSY 357
Db 624 SNSMDTSNDFEETRE---KPIDSVVDEYLSSES-VQKQFGGWTY 663
RESULT 12
S62117
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: S62117; S24423; S17999; S15714; S36388
R:Coffer, P.J.; Woodgett, J.R.
submitted to the EMBL Data Library, December 1991
A:Reference number: S62117
A:Accession: S62117
A:Molecule type: mRNA
A:Residues: 1-480 <COF>
A:Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:G630; PIDN:
A:Note: this is a revision to the sequence from reference S17999
R:Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A:Reference number: S24423; MUID:92249329; PMID:1533586
A:Contents: exratum
A:Accession: S24423
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 70-78, 'N', 80-145 <COM>
A:Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036
A:Note: this is a revision to the sequence from reference S17999
R:Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A:Title: Molecular cloning and characterisation of a novel putative protein-serine kina
A:Reference number: S17999; MUID:92037600; PMID:1718748
A:Accession: S17999
A:Molecule type: mRNA
A:Residues: 1-70, 'TPSSSAACGPRSSASRTWRRPRSGVDHRRPDGRRRAQAGGDDGLPVGLTRRELGRDGGVAGQ
A:Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036
A:Note: this sequence has been revised in references S62117 and S24423
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F:4-106/Domain: pleckstrin repeat homology <PUK>
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict
Query Match 44.2%; Score 863.5; DB 1; Length 480;
Best Local Similarity 48.2%; Pred. No. 5.4e-34;
Matches 174; Conservative 60; Mismatches 112; Indels 15; Gaps 7;
QY 6 ACTPSPQPSRANGINLGPSANPNQAQPT--DFDFLKVIGKNGYKVLAKRSDGAFYAV 63
Db 122 SGSPENSGAEEMESVSL---AKPKRVRTMNEFYEYKLLGKGTGFKGVLLYKKAATAYAM 178
QY 64 KYLOKKSILKKKQSHIMAERSVLLKNVRHPLVGLRYSFQTPPEKLYFVLVDYVNGGELFF 123
Db 179 KILKEVIVAKDEVAHTLTENRV-LQNSRHSLSLTALKYSFQTHDRLCFVMEVANGELFF 237

Qy	124	HLQRRRRFLPPRRFYAAEASAIYLHS-LNIIYRDLKPENILLDCQGHVLTDFGLCK	181
Db	238	HLSSRRVFSEDRARFYGAEIVSALDYLHSEKEVYVRDLKLENMLDKDGHIKITDFGLCK	297
Qy	183	EGVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFYSDVSQM	242
Db	298	EGIKDQATWKTCGTPPEYLAPEVLDDNDYGRAVDWVGGLGVVVMYEMMCGRLPFFYNQDHEKL	357
Qy	243	YENILHQPLQIPGGRVTAAACDLOSLLHDKOORL-GSKADFLFIKNHVFSPINDDLY	301
Db	358	FELLIMEEIRPRTLSPKASLLSGLLKKDPKQRLGGSEDAKEIMQHRFFASIVMQDYY	417
Qy	302	HKRLTPFPNPVNTGPAIDLKHPDPTQAVSKSTGCTPDTVASSSGASSA-----FLGFSY	357
Db	418	EKKLSPPPKQVTSYDTRFYDEEFTAQMITIT---PPDQDDSMEGVDSERRRHPFPFSY	474
Qy	358	A 358	
Db	475	\$ 475	
RESULT 13			
JC2438			
protein kinase (EC 2.7.1.37) akt2 [validated] - rat			
N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific			
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004			
C;Accession: J02438			
R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.			
Biochem. Biophys. Res. Commun. 205, 817-825, 1994			
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their			
A;Reference number: JC2437; MOID:95091823; PMID:7999118			
A;Accession: JC2438			
A;Molecule type: mRNA			
A;Residues: 1-481 <KON>			
A;Cross-references: UNIPROT:P47197; UNIPARC:UPI000012577E; DDBJ:D30041; NID:G41			
A;Experimental source: testis			
C;Function:			
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-			
A;Pathway: signal transduction pathways regulating various processes including			
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology			
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific			
F;4-106/Domain; pleckstrin repeat homology <PLK>			
F;150-409/Domain; protein kinase homology <KIN>			
F;158-166/Region; protein kinase ATP-binding motif			
F;181/Active site; Lys #status predicted			
Query Match 44.1%; Score 862; DB 1; Length 481;			
Best Local Similarity 48.3%; Pred. No. 6.3e-34;			
Matches 172; Conservative 59; Mismatches 113; Indels 12; Gaps 5			
Qy	10	SPOPSRANGNTINLGPS-ANPNAQPTDFDLKVIQKNGYKVLAKRKSQDGFAYAVKVLQK	68
Db	126	SPSDSTSEMMEVAVSKARAKVTWMDFDYLLKLGKTFGKVLVREKATGRYVAMKILRK	185
Qy	69	KSLKKKQSHIMAEKSVLLKNVRHPELVGLRYSFOTPEKLYFVLVYVNGGELFFHLQRE	128
Db	186	EVIIAKDEVAHTVTB-SRVLQNTRHFFLTALKYAFQHRDLRCFMWEYANGDGLFFHLSRE	244
Qy	129	RRLFLPRARFYAAEASAIYLHS-LNIIYRDLKPENILLDCQGHVLTDFGLCKEGVEPE	188
Db	245	RVFTEDRARFYGAEIVSALEYLHSTDVYVRDIKLENMLDKDGHIKITDFGLSKEGISDG	304
Qy	189	DTTSTFCGTPPEYLAPEVLKPEYDRAVDWMCIGAVLYEMLHGLPPFYSDVSQMYENILH	248
Db	305	ATWKTFPCGTPPEYLAPEVLDDNDYGRAVDWVGGLGVVVMYEMMCGRLPFFYNQDHERLFL	364
Qy	249	QPLQIPGGRVTAAACDLOSLLHDKOORL-GSKADFLFIKNHVFSPINDDLYLHKLTP	307
Db	365	ESIRFPRTLGPBKAELLAGLKKDPKQRLGGGSDAKEVMEHRRFFIJSINQDVVQKKLLP	424
Qy	308	PFPNPVNTGPAIDLKHPDPTQAVSKSTGCTPDTVASSSGA-----SSAPLGFSYA	358

Db 425 PFKQVTSVDTRYFDDEFT-----AQSIITTPPDYSLGSLSLDQRTTHFPQFSYS 476

RESULT 14

A38578

protein kinase 2 (EC 2.7.1.1) - slime mold (Dictyostelium discoideum)

C;Species: Dictyostelium discoideum

C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 31-Dec-2004

C;Accession: A38578

R;Haribabu, B.; Dottin, R.P.

Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991

A;Title: Identification of a protein kinase multigene family of Dictyostelium

A;Reference number: A38578; MUID:91142122; PMID:1996312

A;Accession: A38578

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-479 <HAR>

A;Cross-references: UNIPROT:P28178; UNIPARC:UPI0000131B58; GB:M59744; NID:gl677

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serin

F;151-407/Domain: protein kinase homology <KIN>

F;159-167/Region: protein kinase ATP-binding motif

Query Match 43.6%; Score 852; DB 2; Length 479;

Best Local Similarity 46.9%; Pred. No. 1.9e-33;

Matches 175; Conservative 64; Mismatches 118; Indels 16; Gaps 6

QY 3 SSPAGTSPQPSRANGNINLGPSANP-----NAQPTDFDFLKVIGKNGYGVKLLA 52

Db 111 ASNEASSPDSPNGSGNGNDEDEGPEEVFSKNQKQATKDDFELLNVIGKSPGKVMQV 170

QY 53 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPPFLVGLRYSPTPEKLYFV 112

Db 171 KKGEDKIFAMKVLRKDAIARIKQVNHTKSEKTI-LQCISHPFIIVNLHYAFQTKDKLYMV 229

QY 113 LDVYNGGELFFHLQRRERFFLEPRARFYAAEEVASAIGYLHLSUNIYRDLPENILLDCQGH 172

Db 230 LDFVNGGELFFHLKREGFSEPRVKIYAAETVSALDHLHKQDIYVYRDLPENILLDSEGH 289

QY 173 VLTDFGLCKEGVEPEPTTSTFCCTPEVLAPEVLKPEPYDRAVDWVCLGAVLYEMLGLP 232

Db 290 ICITDFGLSKK-IETTDGTTFCGTPYLAPVLNGHGHGCAVDWNSLGTLLYEMLTGLP 348

QY 233 PFYSQDVSYOMYENILHPLQATPGGRTVAACDLLQSLHLKQORQLGSKADFLKKNHVFV 292

Db 349 PFYSQNVSTWYQKILNGELAKITPTVISPEAKSLLEGLLTREVDKRLGKGG-EVKQHPWF 407

QY 293 SPINWDDLYHKRLTPPNPNVNTGPGADLKHPDFEFTQZAVSKSIGCTPTPTVASSGSSAF 352

Db 408 KNIDWEKLDKREVEVHFVKPKVKSCTDISQDPVFTQBRPMDSLVET-SALGDAMGKOTSF 466

QY 353 LGFSYAPEDDDIL 365

Db 467 EGFTYA--DSIL 477

RESULT 15

JS0178

protein kinase YKR2 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein YMR718.03c; protein YMR104c

C;Species: Saccharomyces cerevisiae

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Oct-2004

C;Accession: JS0178; S30904; S54565

R;Kubo, K.; Ohno, S.; Matsumoto, S.; Yahara, I.; Suzuki, K.

Gene 76, 177-180, 1989

A;Title: A novel yeast gene coding for a putative protein kinase.

A;Reference number: JS0178; MUID:89306654; PMID:2663649

A;Accession: JS0178

A;Molecule type: DNA

A;Residues: 1-677 <KUB>

A;Cross-references: UNIPROT:P18961; UNIPARC:UPI0000013BDFP; EMBL:M24929; NID:92

R;Chen, P.; Lee, K.S.; Levitt, D.E.

Mol. Gen. Genet. 236, 443-447, 1993

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2006, 23:08:15 ; Search time 59.7818 Seconds
(without alignments)
4331.236 Million cell updates/sec

Title: US-09-868-131A-1

Perfect score: 1954

Sequence: 1 MNSSPAGTSPQPSRANGNI.....ASSAFLGFSYAPDDDDILDC 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1954	100.0	427	1	SGK2 HUMAN
2	1954	100.0	427	2	Q5H8Y6 HUMAN
3	1947	99.6	367	2	Q5T2R3 HUMAN
4	1943	99.4	393	2	Q52PK5 HUMAN
5	1938.5	99.2	366	2	Q5H8Z1 HUMAN
6	1932	98.9	367	2	Q5RDZ9 PONPY
7	1848	94.6	367	1	SGK2 MOUSE
8	1540	78.8	302	1	SGK2 RAT
9	1497	76.6	285	2	Q5H8Y4 HUMAN
10	1450.5	74.2	350	2	Q4SY9Y TETNG
11	1436	73.5	433	2	Q7ZTW4 BRARE
12	1432	73.3	431	2	Q5QOU5 FUNHE
13	1419	72.6	432	2	Q6ULI9 CHICK
14	1418	72.6	434	2	Q93524 XENLA
15	1416	72.5	431	1	SGK1 RABIT
16	1415	72.4	434	2	Q6GFN6 XENLA
17	1413	72.3	431	2	Q68G05 RAT
18	1411	72.2	418	2	Q5BKX4 XENTR
19	1411	72.2	421	2	Q5TCN4 HUMAN
20	1411	72.2	431	2	Q5TCN3 HUMAN
21	1411	72.2	445	2	Q5TCN2 HUMAN
22	1411	72.2	526	2	Q5V765 HUMAN
23	1409	72.1	431	1	SGK1 MOUSE
24	1409	72.1	519	2	Q6N585 MOUSE
25	1407	72.0	431	1	SGK1 HUMAN
26	1406	72.0	431	2	Q4R633 MACFA
27	1404.5	71.9	430	1	SGK3 RAT
28	1394.5	71.4	490	2	Q4RR91 TETNG
29	1394	71.3	434	2	Q6GLY8 XENLA
30	1392	71.2	594	2	Q73927 SQUAC
31	1390.5	71.2	433	2	Q73926 SQUALUS aca

32 1331.5 68.1 429 2 Q8VEK1 MOUSE
33 1331.5 68.1 496 1 SGK3 MOUSE
34 1323.5 67.7 429 2 Q6FHV7 HUMAN
35 1323.5 67.7 496 1 SGK3 HUMAN
36 1323.5 67.7 496 2 Q53EW6 HUMAN
37 1323.5 67.7 496 2 Q5R7A7 PONPY
38 1320.5 67.6 518 2 Q4SFC2 TETNG
39 1318.5 67.5 496 2 Q5H9Q5 HUMAN
40 1314.5 67.3 490 2 Q5ZJQ4 CHICK
41 1213 62.1 1114 2 Q4SYX7 TETNG
42 1063 54.4 316 2 Q4RI65 TETNG
43 1035 53.0 1550 2 Q4SYI0 TETNG
44 1025.5 52.5 198 2 Q5H8Y5 HUMAN
45 984 50.4 423 2 Q613H2 CAEBR

ALIGNMENTS

RESULT 1
SGK2 HUMAN
ID SGK2 HUMAN STANDARD; PRT; 427 AA.
AC Q9HBY8; Q9UKG6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2).
GN Name=SGK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), PHOSPHORYLATION SITE THR-253, AND MUTAGENESIS OF SER-416.
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel isoforms of serum- and glucocorticoid-induced protein kinase";
RL Biochem. J. 344:189-197(1999).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Leharvaish M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McKay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams S.A., Wilming L., Wray F.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
RL "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
[3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McWan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kretzman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION
RX MEDLINE=22284526; PubMed=12397388; DOI=10.1007/s00424-002-0873-2;
RA Gamber N., Fillon S., Feng Y., Friedrich B., Lang P.A., Henke G.,
RA Huber S.M., Kobayashi T., Cohen P., Lang F.;
RT "K(+) channel activation by all three isoforms of serum- and
RT glucocorticoid-dependent protein kinase SGK.";
RL Pflugers Arch. 445:60-66(2002)
CC -!- FUNCTION: Involved in the activation of potassium channels.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2; Synonyms=beta;
CC IsoId=Q9HY8-1; Sequence=Displayed;
CC Name=1; Synonyms=alpha;
CC IsoId=Q9HY8-2; Sequence=VSP_004932;
CC -!- TISSUE SPECIFICITY: Highly expressed in liver, kidney and
CC pancreas, and at lower levels in brain.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: Not regulated by serum or glucocorticoids.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF186470; AAG17012.1; -; mRNA.
CC EMBL; AF169034; AAF12757.2; -; mRNA.
CC EMBL; Z98752; CAC18509.1; -; Genomic DNA.
CC EMBL; BC014037; AAH14037.2; ALT SEQ: mRNA.
CC EMBL; BC065511; AAH65511.1; -; mRNA.
CC HSSP; P31751; IGZK.
CC Ensembl; ENSG00000101049; Homo sapiens.
CC HGNC; HGNC:13900; SGK2.
CC MIM; 607589; -.
CC GO; GO:0015459; F:potassium channel regulator activity; IDA.
CC GO; GO:0004682; F:protein kinase CK2 activity; NAS.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
CC GO; GO:0017080; F:sodium channel regulator activity; NAS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
CC GO; GO:0007243; P:protein kinase cascade; TAS.
CC GO; GO:0006979; P:response to oxidative stress; TAS.
CC InterPro; IPR00961; Pkinase_C.
CC InterPro; IPR008271; Ser_thr_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00433; Pkinase C; 1.
CC ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 95 352 Protein kinase.
FT NP_BIND 101 109 ATP (by similarity).
FT MOTIF 128 138 Nuclear localization signal (By
FT similarity).
FT ACT_SITE 219 219 Proton acceptor (By similarity).
FT BINDING 124 124 ATP (By similarity).
FT MOD_RES 253 253 Phosphothreonine (by PDPK1).
FT VARSPLIC 1 60 Missing (in isoform 1).
FT FTID=VSP_004932.
FT MUTAGEN 416 416 S->D: Increased activation.
SQ SEQUENCE 427 AA; 47604 MW; D8F0FA6DF54B1370 CRC64;
Query Match 100.0%; Score 1954; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.4e-125;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFELKVGKNGYKVLAKRKSDGAF 60
DB 61 MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFELKVGKNGYKVLAKRKSDGAF 120
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120
DB 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 180
QY 121 LFFHLQRRERFLEPRARFYAAEVAISAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
DB 181 LFFHLQRRERFLEPRARFYAAEVAISAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240
QY 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDVYS 240
DB 241 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDVYS 300
QY 241 QMYENILHQPLOIPGGRVTAACDLQLSLHKDQRLGSKADFLKKNHVFSPINWDDL 300
DB 301 QMYENILHQPLOIPGGRVTAACDLQLSLHKDQRLGSKADFLKKNHVFSPINWDDL 360
QY 301 YHKRLTPFPNPNVTGPADLKHPDPEFTQEAHSVSKSGCTPDTVASSSGASSAFGLGSYAPE 360
DB 361 YHKRLTPFPNPNVTGPADLKHPDPEFTQEAHSVSKSGCTPDTVASSSGASSAFGLGSYAPE 420
QY 361 DDIDLC 367
DB 421 DDIDLC 427
RESULT 2
QSH8Y6 HUMAN
ID QSH8Y6_HUMAN PRELIMINARY; PRT; 427 AA.
AC QSH8Y6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE OTTHUMP00000031703.
GN Name=SGK2; ORFNames=RPL-138B7.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1] NUCLEOTIDE SEQUENCE.
RP Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z98752; CAI42312.1; -; Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00433; Pkinase C; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 427 AA; 47604 MW; D6F0FA6DF54B1370 CRC64;

Query Match 100.0%; Score 1954; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.4e-125;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGKLLAKRKS DGAF 60
DB 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGKLLAKRKS DGAF 120
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 120
DB 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 180
QY 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSINIYRDLKPNILLDCQGHVLTDFGL 180
DB 181 LFFHLQRRERFLPRARFYAAEVASAIYGLHSINIYRDLKPNILLDCQGHVLTDFGL 240
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWVWCLGAVLYEMLHGLPFPYSDVS 240
DB 241 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWVWCLGAVLYEMLHGLPFPYSDVS 300
QY 241 QMYENILHQLQIPGRTVAACDLQLSLHKDQORQLGSKADFLKKNHFFSPINWDDL 300
DB 301 QMYENILHQLQIPGRTVAACDLQLSLHKDQORQLGSKADFLKKNHFFSPINWDDL 360
QY 301 YHKRLTPPNPNVTGPADLKHPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
DB 361 YHKRLTPPNPNVTGPADLKHPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
DB 421 DDDILDC 427

RESULT 3
Q52R3 HUMAN PRELIMINARY; PRT; 367 AA.
ID Q52R3 HUMAN PRELIMINARY; PRT; 367 AA.
AC Q52R3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serum/glucocorticoid regulated kinase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
RT vector.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT020098; AAV38901.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00433; Pkinase C; 1.
DR SMART; SM000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Kinase.
SQ SEQUENCE 367 AA; 41233 MW; C91DD892C4C2486B CRC64;

Query Match 99.6%; Score 1947; DB 2; Length 367;
Best Local Similarity 99.7%; Pred. No. 1.1e-124;
Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGKLLAKRKS DGAF 60
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGKLLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 120
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 120
QY 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSINIYRDLKPNILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSINIYRDLKPNILLDCQGHVLTDFGL 180
QY 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWVWCLGAVLYEMLHGLPFPYSDVS 240
DB 181 CKEGVEPEDTTSTFCGTPEYLAPEVLKRPYDRAVDWVWCLGAVLYEMLHGLPFPYSDVS 240
QY 241 QMYENILHQLQIPGRTVAACDLQLSLHKDQORQLGSKADFLKKNHFFSPINWDDL 300
DB 241 QMYENILHQLQIPGRTVAACDLQLSLHKDQORQLGSKADFLKKNHFFSPINWDDL 300
QY 301 YHKRLTPPNPNVTGPADLKHPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
DB 301 YHKRLTPPNPNVTGPADLKHPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 361 DDDILDC 367
DB 361 DDDILDC 367

RESULT 4
Q52PK5 HUMAN PRELIMINARY; PRT; 393 AA.
ID Q52PK5 HUMAN PRELIMINARY; PRT; 393 AA.
AC Q52PK5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serum/glucocorticoid regulated kinase 2.
GN Name=SGK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Li H., Nong W., Zhou G., Ke R., Shen C., Zhong G., Zheng Z., Liang M.,
RA Xiao W., Lin L., Yang S.;
RT "Direct Submission.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

EMBL; AY987010; AAX88805.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot Kinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase C; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TyrKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Kinase.
 SQ SEQUENCE 393 AA; 43962 MW; B9931E71A8B998D6 CRC64;

Query Match 99.4%; Score 1943; DB 2; Length 393;
 Best Local Similarity 99.5%; Pred. No. 2.3e-124;
 Matches 365; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAOPTDFDLKVIKGNVGVLLAKRKS DGAF 60
 DB 27 MNSSPAGTSPQPSRANGNINLGPSANPNAOPTDFDLKVIKGNVGVLLAKRKS DGAF 86
 QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120
 DB 87 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 146
 QY 121 LFFHLQRRRFLPEPRARFYAAEVAASAI GYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
 DB 147 LFFHLQRRRFLPEPRARFYAAEVAASAI GYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 206
 QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDVS 240
 DB 207 CKEGVEPEDTTSTFCGTPPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDVS 266
 QY 241 QMYENILHQPLOIPGRTVAACDLQLSLHKKQORQLGSKADFLEIKNHVFFSPINWDDL 300
 DB 267 QMYENILHQPLOIPGRTVAACDLQLSLHKKQORQLGSKADFLEIKNHVFFSPINWDDL 326
 QY 301 YHKRLTPFPNPNVTGPADLKHFDPFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
 DB 327 YHKRLTPFPNPNVTGPADLKHFDPFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 386
 QY 361 DDDILDC 367
 DB 387 DDDILDC 393

RESULT 5
 QSH8Z1_HUMAN
 ID QSH8Z1_HUMAN PRELIMINARY; PRT; 366 AA.
 AC QSH8Z1;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE OTTHUMP00000031706.
 GN Name=SGK2; ORFNames=RP1-13887.2-006;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Beasley H.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

EMBL; Z98752; CAI42315.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot Kinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase C; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TyrKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 SQ SEQUENCE 366 AA; 41047 MW; 8B8546894C23571F CRC64;

Query Match 99.2%; Score 1938.5; DB 2; Length 366;
 Best Local Similarity 99.7%; Pred. No. 4.2e-124;
 Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAOPTDFDLKVIKGNVGVLLAKRKS DGAF 60
 DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAOPTDFDLKVIKGNVGVLLAKRKS DGAF 60
 QY 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 120
 DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGE 119
 QY 121 LFFHLQRRRFLPEPRARFYAAEVAASAI GYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
 DB 120 LFFHLQRRRFLPEPRARFYAAEVAASAI GYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 179
 QY 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDVS 240
 DB 180 CKEGVEPEDTTSTFCGTPPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFSQDVS 239
 QY 241 QMYENILHQPLOIPGRTVAACDLQLSLHKKQORQLGSKADFLEIKNHVFFSPINWDDL 300
 DB 240 QMYENILHQPLOIPGRTVAACDLQLSLHKKQORQLGSKADFLEIKNHVFFSPINWDDL 299
 QY 301 YHKRLTPFPNPNVTGPADLKHFDPFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
 DB 300 YHKRLTPFPNPNVTGPADLKHFDPFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 359
 QY 361 DDDILDC 367
 DB 360 DDDILDC 366

RESULT 6
 QSRDZ9_PONPY
 ID QSRDZ9_PONPY PRELIMINARY; PRT; 367 AA.
 AC QSRDZ9;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein DKFZp469N2435.
 GN Name=DKFZp469N2435;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RG The German cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,

```
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857741; CAH90008.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase C.
DR Pfam; PF00433; Pkinase C. 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 367 AA; 41218 MW; 61128B6CC0519B73 CRC64;

Query Match          98.9%; Score 1932; DB 2; Length 367;
Best Local Similarity 98.6%; Pred. No. 1.2e-123;
Matches 362; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAPQPTDFPLKVGKNGYKVLAKRKSDGAF 60
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNAPQPTDFPLKVGKNGYKVLAKRKSDGTF 60

QY 61 YAVKVLQKSLKAKKQSHIMAFSLVLLKNVRPELVGLRYSPOTPEKLYFVLVDYNGGE 120
DB 61 YAVKVLQKSLKAKKQSHIMAFSLVLLKNVRPELVGLRYSPOTPEKLYFVLVDYDGE 120

QY 121 LFPHLQRRERFLPRFARFYAAEVAASAIQYLHSLNIYRDLKPNILLDCQGHVVLDFGL 180
DB 121 LFPHLQRRERFLPRFARFYAAEVAASAIQYLHSLNIYRDLKPNILLDCQGHVVLDFGL 180

QY 181 CKEGVPEPTTSTFCGTPEYLAPEVLRKPEYDRAVDWVCLGAVLYEMLHGLPFYSDVS 240
DB 181 CKEGVPEPTTSTFCGTPEYLAPEVLRKPEYDRAVDWVCLGAVLYEMLHGLPFYSDVS 240

QY 241 QMYENILHPLQIPGGRTWAAACDLQSLHKQORQLGSKADFLKKNHVFSPINWDDL 300
DB 241 QMYENILHPLQIPGGRTWAAACDLQSLHKQORQLGSKADFLKKNHVFSPINWDDL 300

QY 301 YHKRLTPFPNPNVTGPGADLKHFPDPEPTQEA VSKSIGCTPDTVASSGASAFGLGFSYAPE 360
DB 301 YHKRLTPFPNPNVAGPADLKHFPDPEPTQEA VSKSIGCTPDTVASSGASAFGLGFSYAPE 360

QY 361 DDILDC 367
DB 361 DDILDC 367

RESULT 7
SGK2_MOUSE
ID SGK2_MOUSE STANDARD; PRT; 367 AA.
AC Q9QZS5; Q8R0P6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2).
GN Name=Sgk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Tesdale R.D., Tonita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Involved in the activation of potassium channels (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9QZS5-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9QZS5-2; Sequence=VSP_004933;
CC Note=No experimental confirmation available;
```

```
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: Not regulated by serum or glucocorticoids.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF169033; AAF12756.1; -; mRNA.
DR EMBL; AK050009; BAC34031.1; -; mRNA.
DR EMBL; BC026549; AAH26549.1; -; mRNA.
DR HSSP; P31751; 1GZK.
DR Ensembl; ENSMUSG0000017868; Mus musculus.
DR MGI; MGI:1351318; Sgk2.
DR GO; GO:0015459; F:potassium channel regulator activity; ISS.
DR GO; GO:0004682; F:protein kinase CK2 activity; ISS.
DR GO; GO:0017080; F:sodium channel regulator activity; ISS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 35 292 Protein kinase.
FT NP_BIND 41 49 ATP (By similarity).
FT MOTIF 68 78 Nuclear localization signal (By
FT similarity).
FT ACT_SITE 159 159 Proton acceptor (By similarity).
FT BINDING 64 64 ATP (By similarity).
FT MOD_RES 193 193 Phosphothreonine (by PDPK1) (By
FT similarity).
FT VARSPLIC 171 199 Missing (in isoform 2).
FT CONFLICT 77 77 /FTId=VSP_004933.
FT SEQUENCE 367 AA; 41359 MW; 668C04B1A1E9E33A CRC64;
Query Match 94.6%; Score 1848; DB 1; Length 367;
Best Local Similarity 94.3%; Pred. No. 6.3e-118;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNGYKVLAKRKSDDGAF 60
DB 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNGYKVLAKRKSDDGAF 60
QY 61 YAVKVLQKSLKXKEQSHMAERSVLLKNVRHPLVGLRYSFQTEPKLYFVLVDYNGGE 120
DB 61 YAVKVLQKSLKXKEQSHMAERNVLLKNVRHPLVGLRYSFQTEPKLYFVLVDYNGGE 120
QY 121 LFFHLQRRRFLPEPRARFYAAEVASAIQVLSHLSNIYYRDLKPEINILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRRFLPEPRARFYAAEVASAIQVLSHLSNIYYRDLKPEINILLDCQGHVLTDFGL 180
QY 181 CKGEVPEPTTSTFCTPYLAPEVLRLKEPYDRAVDWVCLGAVLYEMLHGLPPFPYSQDVS 240
DB 181 CKCEVPEPTTSTFCTPYLAPEVLRLKEPYDRAVDWVCLGAVLYEMLHGLPPFPNTDVA 240
QY 241 QMVENILHQLQIPGGRVTAACDLLOSILHKKORQLGSKADFELEIKNVHFFSPINWDDL 300
DB 241 QMVENILHQLQIPGGRVTAACDLLOSILHKKORQLGSKEDFLDIKNHFFSPINWDDL 300
QY 301 YHKRLTPPPNPNVTGPDALKHDFEPTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 360
DB 301 YHKRLTPPPNPNVEGPADLKHDFEPTQBAVSKSIGCTPDTVASSSGASSAFILGFSYADQ 360
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QY 361 DDDILD 366
DB 361 DDDILD 366
RESULT 8
ID SGK2 RAT STANDARD; PRT; 302 AA.
AC Q8RAU9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2) (Fragment).
GN Name=Sgk2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Feng Y.X., Huber S.M., Waerntges S., Lang F.;
RT "SGK2 and SGK3 mRNA expression in rat kidney.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the activation of potassium channels (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF361756; AAL91351.1; -; mRNA.
DR HSSP; P31751; 1GZK.
DR Ensembl; ENSRNOG00000033573; Rattus norvegicus.
DR RGD; 620232; Sgk2.
DR GO; GO:0015459; F:potassium channel regulator activity; ISS.
DR GO; GO:0004682; F:protein kinase CK2 activity; ISS.
DR GO; GO:0017080; F:sodium channel regulator activity; ISS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 18 275 Protein kinase.
FT NP_BIND 24 32 ATP (By similarity).
FT MOTIF 51 61 Nuclear localization signal (By
FT similarity).
FT ACT_SITE 142 142 Proton acceptor (By similarity).
FT BINDING 47 47 ATP (By similarity).
FT MOD_RES 176 176 Phosphothreonine (by PDPK1) (By
FT similarity).
FT NON_TER 1 1
FT NON_TER 302 302
FT SEQUENCE 302 AA; 34622 MW; A74EB3F424283D66 CRC64;
Query Match 78.8%; Score 1540; DB 1; Length 302;
Best Local Similarity 94.7%; Pred. No. 5e-97;
Matches 286; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
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QY 18 GNINLGPSANPNAQPTDFDLKVLGKNGYKVKLLAKRKSAGAYAVKVLQKKSILKKKEQ 77
 Db 1 GNINLGPSANPNAQPTDFDLKVLGKNGYKVKLLAKRKSAGAYAVKVLQKKSILKKKEQ 60
 QY 78 SHIMASRVLKKNRHPFLVGLRYSQTPEKLYFVLDYVNGGELFHLQREPRFLPRAR 137
 Db 61 SHIMASRVLKKNRHPFLVGLRYSQTPEKLYFVLDYVNGGELFHLQREPRFLPRAR 120
 QY 138 FYAAEVASAIYGLHSLNIIYRDLKPNILLLDCCGHVVLTDGFLCKEVEPEPTTSTFCGT 197
 Db 121 FYAAEVASAIYGLHSLNIIYRDLKPNILLLDCCGHVVLTDGFLCKEVEPEPTTSTFCGT 180
 QY 198 PEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVSQMYENILHQLQIPGGR 257
 Db 181 PEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVSQMYENILHQLQIPGGR 240
 QY 258 TVAACDLQLSLHKKDQORLQSGKADFLKINKNHVFSPINWDDLYHKLTPPENPNVTGPA 317
 Db 241 TVAACDLQLSLHKKDQORLQSGKEDFLDKNHFSPINWDDLYHKLTPPENPNVEGPA 300
 QY 318 DL 319
 Db 301 DL 302
 RESULT 9
 Q5H8Y4 HUMAN
 ID Q5H8Y4 HUMAN PRELIMINARY; PRT; 285 AA.
 AC Q5H8Y4
 DT 10-MAY-2005 (TEMBLrel. 30, Created)
 DT 10-MAY-2005 (TEMBLrel. 30, Last sequence update)
 DE OTTHUMP0000031704.
 GN Name=SGK2; ORFNames=RPL-138B7.2-004;
 OS Homo sapiens, (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Beasley H.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; Z98752; CAI42314.1; -; Genomic_DNA.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 285 AA; 32130 MW; A3493A701ABB4542 CRC64;
 Query Match 76.6%; Score 1497; DB 2; Length 285;
 Best Local Similarity 99.6%; Pred. No. 4e-94;
 Matches 283; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVLGKNGYKVKLLAKRKSAGAF 60
 Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVLGKNGYKVKLLAKRKSAGAF 60

RESULT 10 Q4S7Y9 TETNG

ID Q4S7Y9 TETNG PRELIMINARY; PRT; 350 AA.
 AC Q4S7Y9;
 DT 13-SEP-2005 (TEMBLrel. 31, Created)
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
 DE Chromosome 9 SCAF14710, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG0002577001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
 cycle. It is required in higher cells for entry into S-phase and
 mitosis. Component of the kinase complex that phosphorylates the
 repetitive C-terminus of RNA polymerase II. Catalytic component of
 MPF (By similarity).
 CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
 mature oocytes (By similarity).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; CAEE01014710; CAG03243.1; -; Genomic_DNA.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.

QY 358 APEDDDIL 365
DB 426 APAMDYL 433

RESULT 12

Q5Q0U5_FUNHE PRELIMINARY; PRT; 431 AA.
ID Q5Q0U5_FUNHE
AC Q5Q0U5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serum and glucocorticoid-regulated kinase.
GN Name=SGK;
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OC NCBI_TaxID=8078;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Sato J.D., Clarke C.C., Stanton B.A.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY800243; AAV80429.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase C.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 431 AA; 48870 MW; 91C80821F64B454D CRC64;

Query Match 73.3%; Score 1432; DB 2; Length 431;
Best Local Similarity 72.0%; Pred. No. 1.8e-89;
Matches 265; Conservative 47; Mismatches 48; Indels 8; Gaps 3;
QY 1 MNSSPAGTSPQPSRANGNINILGSPANPAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60
DB 69 MNSNP--SPPPSPSQ---QINLGSSNPSPAKSDPHFLKVIKGNVGVLLAKRHTDDQF 123
QY 61 YAVKVLQKSLKKKEQSHMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLVDYNGGE 120
DB 124 YAVKVLQKALKKKEKHMSERNVLLKNVHPLVGLHYSFQTADKLYFVLVDYNGGE 183
QY 121 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPENILLDQGHVLTDFGL 180
DB 184 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPENILLDQGHVLTDFGL 243
QY 181 CKGEVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMLHGLPPFYSDVS 240
DB 244 CKENIEHNGTSTFCGTPPEYLAPEVLHQPYDRTVDWVWCLGAVLYEMLHGLPPFYSDVS 303
QY 241 QMVENILHQPLOIPGGRITVAACDLQSLHKKDQRLGSKADFLKKNHVFSPINWDDL 300
DB 304 EMDNINLKPLQKPNISNARHLLGGLQKRTKLGKDDFTKIKNHVFSPINWDDL 363
QY 301 YHKRLTTPPNVNTGPDALKHFDPEFTQEAIVSKSIQCTPD---TVASSSGASSAFILGFSY 357

DB 364 NAKKMTTPFPNPNVTGPNDLRHFDEPVPSSIGCSPDCALATASIKEAAAEAFVGSY 423
QY 358 APEDDDIL 365
DB 424 APSMDSYL 431
RESULT 13
Q6ULI9_CHICK PRELIMINARY; PRT; 432 AA.
ID Q6ULI9_CHICK
AC Q6ULI9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Serum-and glucocorticoid-induced kinase.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Malkiewicz S.A., Porter T.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY380825; AAQ88435.1; -; mRNA.
DR HSP; P05132; IATP.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase C; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 432 AA; 48890 MW; 83AB52AFF2609953 CRC64;

Query Match 72.6%; Score 1419; DB 2; Length 432;
Best Local Similarity 71.2%; Pred. No. 1.4e-88;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;
QY 1 MNSSPAGTSPQPSRANGNINILGSPANPAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 60
DB 70 MNSNP--SPPPSPSQ---QINLGSSNPSPAKSDPHFLKVIKGNVGVLLAKRKAEEQF 124
QY 61 YAVKVLQKSLKKKEQSHMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLVDYNGGE 120
DB 125 YAVKVLQKALKKKEKHMSERNVLLKNVHPLVGLHYSFQTADKLYFVLVDYNGGE 184
QY 121 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPENILLDQGHVLTDFGL 180
DB 185 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPENILLDQGHVLTDFGL 244
QY 181 CKGEVEPEDTSTFCGTPPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMLHGLPPFYSDVS 240
DB 245 CKENIEHNGTSTFCGTPPEYLAPEVLHQPYDRTVDWVWCLGAVLYEMLHGLPPFYSDVS 304
QY 241 QMVENILHQPLOIPGGRITVAACDLQSLHKKDQRLGSKADFLKKNHVFSPINWDDL 300
DB 305 EMDNINLKPLQKPNISNARHLLGGLQKRTKLGKDDFTKIKNHVFSPINWDDL 364
QY 301 YHKRLTTPPNVNTGPDALKHFDPEFTQEAIVSKSIQCTPDTV---ASSSGASSAFILGFSY 357

Db 365 INKKTTPPNVNSGSDLRHDPDPTDPEVNSIGQSPDSILITASVKAEAEFLGFSY 424
Qy 358 APEDDDIL 365
Db 425 APVDSFL 432

RESULT 14

O93524 XENLA
ID O93524 XENLA PRELIMINARY; PRT; 434 AA.
AC O93524;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Renal tubule;
RX MEDLINE=99162637; PubMed=10051674; DOI=10.1073/pnas.96.5.2514;
RA Chen S.-Y., Bhargava A., Mastroberardino L., Meijer O.C., Wang J.,
Buse P., Firestone G.L., Verrey F., Pearce D.;
RT "Epithelial sodium channel regulated by aldosterone-induced protein
sgk.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:2514-2519(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Renal tubule;
RA Chen S.-Y., Pearce D.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and
monomeric catalytic subunit). Translocates into the nucleus
(monomeric catalytic subunit) (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC EMBL; AF057138; AAC62398.1; -; mRNA.
DR HSSP; P31751; 1MRV.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Cell cycle; Cell division; Hypothetical protein; Kinase;
KW Nuclear protein; Nucleotide-binding; Serine/threonine-protein kinase;
KW Transferase; CAMP.
SQ SEQUENCE 434 AA; 49130 MW; 4A061E38B6AA6F61 CRC64;

Query Match 72.6%; Score 1418; DB 2; Length 434;
Best Local Similarity 70.3%; Pred. No. 1.6e-88;
Matches 258; Conservative 57; Mismatches 42; Indels 10; Gaps 2;

Qy 2 NSSPACTPSPSANGNTNLGSPANPNAQPTDFDLKVIKGNVGVLLAKRKSGAFY 61
Db 75 NSSPPSPSQ-----INLGSSNPHPAKPSDFQLKIIGKSGFKVLLARHQDEKEY 127
Qy 62 AVKVLQKKILKKKEQSHMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLVDYNGGRL 121
Db 128 AVKVLQKKALKKKEKHIMSERNVLLKNVHPFLVGLHFSQTTSRLYFILDYINGGRL 187

Qy 122 PHLQRRERFLEPRARFYAAEVAASIGYLHSLNIITYRDLKPNILLDCQGHVVLTDGFLC 181
Db 188 FYHLQRRERCFLEPRARFYAAETASALGYLHSLNIITYRDLKPNILLDSQGHVVLTDGFLC 247
Qy 182 KEGVEPEDTSTFCGTPPEYLAPVLRKEPYDRAVDWGLGAVLYEMLHGLPPFPYSODVSQ 241
Db 248 KENIEPNGTSTFCGTPPEYLAPVLRKEPYDRTVDWGLGAVLYEMLYGLPFPYSSENTAE 307
Qy 242 MYENILHQLPQIPGGRTVAACDLLQSLHLHKQORGLSKADFLKINHNHVFSPINWDDLY 301
Db 308 MYDNLINKPLQLKPNITNSARNLLGLLQKDKRTKRGAKNDFMEIKNHIFFPINWDDLI 367
Qy 302 HKRLTPPNPNVTGADLKHDPPEETOAVSISICTPTDV--ASSSGASAFGLGFSYA 358
Db 368 NKKITPPPNPNVSGPSDLQHFDEPTEBPVNSIGQSPDSILITASKEAAEAFMGFSYA 427
Qy 359 PEDDDIL 365
Db 428 PPMESYL 434

RESULT 15

SGK1 RABIT
ID SGK1 RABIT STANDARD; PRT; 431 AA.
AC Q9XTI8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk1 (EC 2.7.1.37)
DE (Serum/glucocorticoid-regulated kinase 1).
GN Name=SGK; Synonyms=SGK1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=New Zealand white;
RX MEDLINE=99287894; PubMed=10358046; DOI=10.1074/jbc.274.24.16973;
RA Naray-Fejes-Toth A., Canessa C., Cleaveland E.S., Aldrich G.,
Fejes-Toth G.;
RT "sgk is an aldosterone-induced kinase in the renal collecting duct.
Effects on epithelial Na+ channels.";
RL J. Biol. Chem. 274:16973-16978(1999).
CC -1- FUNCTION: Protein kinase that plays an important role in
activating certain potassium, sodium, and chloride channels,
suggesting an involvement in the regulation of processes such as
cell survival, neuronal excitability, and renal sodium excretion.
CC May be a key component of cellular stress response. Phosphorylates
NEBD4L, which leads to its inactivation and to the subsequent
activation of various channels and transporters such as ENAC,
Kv1.3, or EAAT1 (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts with NEBD4 and NEBD4L (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear, upon
phosphorylation (By similarity).
CC -1- PTM: Regulated by phosphorylation. Phosphoinositide 3-kinase (PI3-
kinase) pathway promotes phosphorylation at Ser-422 which in turn
increases the phosphorylation of Thr-256 by PDPK1 (By similarity).
CC -1- PTM: Ubiquitinated by NEBD4L; which promotes proteasomal
degradation (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; AF139639; AAD43303.1; -; mRNA.
DR HSSP; P31751; 1GZK.
DR InterPro; IPR000961; Pkinase_C.

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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:06:05 ; Search time 65.3214 Seconds
(without alignments)
2468.595 Million cell updates/sec

Title: US-09-868-131A-3
Perfect score: 1959
Sequence: 1 MASSPVGVSPQPSRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_21.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001s.*
 - 5: Geneseq2002s.*
 - 6: Geneseq2003as.*
 - 7: Geneseq2003bs.*
 - 8: Geneseq2004s.*
 - 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1959	100.0	367	3	AAY95277 Mouse ser
2	1959	100.0	367	7	ADD45797 Rat Prote
3	1848	94.3	367	3	AAY95275 Human ser
4	1848	94.3	367	4	AAY95275 Human ser
5	1848	94.3	367	5	AAD28087 Novel hum
6	1848	94.3	367	5	AAE22765 Human ser
7	1848	94.3	367	8	ADD45799 Human Pro
8	1848	94.3	367	8	ADI29317 Human MAR
9	1848	94.3	367	8	ADJ45521 LXR-ligan
10	1848	94.3	367	8	ADJ45521 Human pro
11	1848	94.3	396	9	ADY37607 Lung canc
12	1848	94.3	427	8	AAY95276 Human ser
13	1848	94.3	427	8	ADQ88284 Human 549
14	1674.5	85.5	367	4	AAE65708 Novel pro
15	1660.5	84.8	398	6	ADA05780 Human NOV
16	1615	82.4	398	8	ADN62944 Human NOV
17	1615	82.4	319	8	AAE99838 AGC prote
18	1606	82.0	335	8	ADJ38886 SGK2 amin
19	1583	80.8	330	8	ADP29822 Human sec
20	1389	70.9	431	3	ADN61463 Human KPP
21	1389	70.9	431	3	AB24116 Rat serum
22	1389	70.9	431	3	AAY95530 A rat ser
23	1387	70.8	407	7	ADC69794 Human ser
24	1387	70.8	431	2	AAW90139 Human sgk
	1387	70.8	431	6	ADA10889 Human cdn

ALIGNMENTS

RESULT 1

AA95277

ID AAY95277 standard; protein; 367 AA.

XX

AC AAY95277;

DT 12-SEP-2000 (first entry)

XX

DE Mouse serum and glucocorticoid-induced protein kinase 2.

XX

KW Serum and glucocorticoid-induced protein kinase 2; SGK2; mouse;

KW phosphorylation; cancer; diabetes; ischaemia; therapy.

XX

OS Mus musculus.

XX

XX WO200035946-A1.

XX

PD 22-JUN-2000.

XX

PF 14-DEC-1999; 99WO-GE004232.

XX

PR 14-DEC-1998; 98US-0112217P.

PR 19-AUG-1999; 99GB-00019676.

XX

XX (UYDU-) UNIV DUNDEE.

XX

XX Cohen P, Kobayashi T, Deak M;

XX

XX WPI; 2000-442364/38.

XX

XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by

XX phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)

XX or dephosphorylation, useful for treatment of cancer, diabetes and

XX ischaemic diseases.

XX

XX Disclosure; Page 7; 127pp; English.

XX

XX The present sequence is that of mouse serum and glucocorticoid-induced

XX protein kinase (SGK) isoform 2, a protein activated by phosphorylation.

XX The invention provides methods of activating SGK (see also AAY95275-79)

XX by phosphorylation using 3-phosphoinositide-dependent protein kinase-1

XX (PDK1), and of reducing the activity of SGK by dephosphorylation. The

XX invention also provides a method of identifying a compound that modulates

XX the activity of SGK. Such compounds are useful for treating patients or

XX requiring modulation of SGK, such as patients with cancer, diabetes or

XX ischaemic disease

XX

SQ Sequence 367 AA;
Query Match 100.0%; Score 1959; DB 3; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.5e-188;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASSPVGVSPQPSRANGNINLGPANPNARPTDFDLKVIKGNKGVLLAKRKS DGAF 60
Db 1 MASSPVGVSPQPSRANGNINLGPANPNARPTDFDLKVIKGNKGVLLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
Db 121 LFFHLQRRERFLPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
QY 181 CKECVEPEETTSFCTGTPPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFFNTDVA 240
Db 181 CKECVEPEETTSFCTGTPPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFFNTDVA 240
QY 241 QMYENILHQPLOIPGGRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
Db 241 QMYENILHQPLOIPGGRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
QY 301 YHKRLTPFPNPNVEGPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
Db 301 YHKRLTPFPNPNVEGPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
QY 361 DDDILDS 367
Db 361 DDDILDS 367

RESULT 2
ADD45797
ID ADD45797 standard; protein; 367 AA.
XX ADD45797;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAF12756, SEQ ID NO 11466.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
FN WO2003016475-A2.
PN
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; AAF12756.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 367 AA;

Query Match 100.0%; Score 1959; DB 7; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.5e-188;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASSPVGVSPQPSRANGNINLGPANPNARPTDFDLKVIKGNKGVLLAKRKS DGAF 60
Db 1 MASSPVGVSPQPSRANGNINLGPANPNARPTDFDLKVIKGNKGVLLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
Db 121 LFFHLQRRERFLPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
QY 181 CKECVEPEETTSFCTGTPPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFFNTDVA 240
Db 181 CKECVEPEETTSFCTGTPPEYLAPEVLKRPYDRAVDWCLGAVLYEMLHGLPPFFNTDVA 240
QY 241 QMYENILHQPLOIPGGRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
Db 241 QMYENILHQPLOIPGGRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
QY 301 YHKRLTPFPNPNVEGPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
Db 301 YHKRLTPFPNPNVEGPADLKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
QY 361 DDDILDS 367
Db 361 DDDILDS 367
RESULT 3
AAV95275
ID AAV95275 standard; protein; 367 AA.
XX
AC AAV95275;
XX
DT 12-SEP-2000 (first entry)
XX
DE Human serum and glucocorticoid-induced protein kinase 2-alpha.
XX

KW Serum and glucocorticoid-induced protein kinase 2; SGK2-alpha; human;
KW phosphorylation; cancer; diabetes; ischaemia; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Modified-site 279
FT /note= "O-phosphorylated"
FT Modified-site 334
FT /note= "O-phosphorylated"
XX
XX
XX WO200035946-A1.
XX
XX 22-JUN-2000.
XX
XX 14-DEC-1999; 99WO-GB004232.
XX
XX 14-DEC-1998; 98US-0112217P.
XX 19-AUG-1999; 99GB-00019676.
XX
XX (UYDU-) UNIV DUNDEE.
XX
XX Cohen P, Kobayashi T, Deak M;
PI WPI; 2000-442364/38.
XX N-PSDB; AAA27856.
XX
XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)
PT or dephosphorylation, useful for treatment of cancer, diabetes and
XX ischemic diseases.
XX
XX Disclosure; Page 6; 127pp; English.
XX
XX The present sequence is that of human serum and glucocorticoid-induced
CC protein kinase (SGK) isoform 2-alpha. SGK (see AAY95279) was initially
CC identified as a glucocorticoid and osmotic stress-responsive gene. Novel
CC isoforms, SGK2 and SGK3, were isolated from EST database searches, and 2
CC splice variants of SGK2, i.e. SGK2-alpha and -beta (see AAY95276), which
CC contains an extra 60 N-terminal residues, were identified. SGK2-alpha is
CC expressed in liver, kidney, pancreas and brain. It is activated by
CC phosphorylation in a similar manner to SGK. The invention provides
CC methods of activating SGK activity by phosphorylation using 3-
CC phosphoinositide-dependent protein kinase-1 (PDK1), and of reducing the
CC activity of SGK by dephosphorylation. The invention also provides a
CC method of identifying a compound that modulates the activity of SGK. Such
CC compounds are useful for treating patients requiring modulation of SGK,
CC such as patients with cancer, diabetes or ischaemic disease
XX
XX Sequence 367 AA;
Query Match 94.3%; Score 1848; DB 3; Length 367;
Best Local Similarity 94.3%; Pred. No. 2.5e-177;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 MASSPVGVSPQPSRANGINLGPANPNARPTDFLKVIGKNGYKVKLLAKRKSDDGAF 60
DB 1 MNSSPAGTSPQPSRANGINLGPANPNARPTDFLKVIGKNGYKVKLLAKRKSDDGAF 60
QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPFLVGLRYSFQTPPEKLYFVLDYVNGGE 120
DB 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPFLVGLRYSFQTPPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLPRARFYTAEVASAIYGLHSLNIYRDLPENILLDCQGHVLLTDFGL 180
DB 121 LFFHLQRRERFLPRARFYTAEVASAIYGLHSLNIYRDLPENILLDCQGHVLLTDFGL 180
QY 181 CKEGVEPEPTSTFCGTPEYLAPEVLKPEYRAVDWMCIGAVLYEMLHGLPFFFTDVA 240
DB 181 CKEGVEPEPTSTFCGTPEYLAPEVLKPEYRAVDWMCIGAVLYEMLHGLPFFFTDVA 240
QY 241 QMYENILHQPLOTIPGGRTVAAACDQLLQSLHLKQORQLGSKADFLDKIKNHFVSPINWDDL 300

Db 241 QMYENILHQPLOTIPGGRTVAAACDQLLQSLHLKQORQLGSKADFLDKIKNHFVSPINWDDL 300
QY 301 YHKRLTPPNPNVVEGPAADLKHFDPFTQEAIVSKSIGCTPDTVASSGASAFLGFSYAQD 360
Db 301 YHKRLTPPNPNVVEGPAADLKHFDPFTQEAIVSKSIGCTPDTVASSGASAFLGFSYAQD 360
QY 361 DDDILD 366
Db 361 DDDILD 366
RESULT 4
AAU28087
ID AAU28087 standard; protein; 367 AA.
XX
AC AAU28087;
XX
DT 19-DEC-2001 (first entry)
XX
DE Novel human secretory protein, Seq ID No 256.
XX
XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.
XX
OS Homo sapiens.
XX
XX WO200166689-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US004942.
XX
PR 07-MAR-2000; 2000US-00519705.
PR 19-MAY-2000; 2000US-00574454.
PR 17-JUN-2000; 2000US-00596193.
PR 14-JUL-2000; 2000US-00616847.
PR 19-SEP-2000; 2000US-00665363.
PR 20-OCT-2000; 2000US-00693267.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX
DR WPI; 2001-589934/66.
DR N-PSDB; AAS44987.
XX
PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis and treatment of
PT cancer, neurological, inflammatory, and autoimmune disorders.
XX
PS Example 4; SEQ ID NO 256; 107pp; English.
XX
XX The invention relates to novel isolated human secreted polypeptides (I)
CC and polynucleotides (II). (I) and (II) are useful for treating
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
CC involved in increasing haematopoiesis, stem cell survival, bone growth
CC and remodeling. (I), (II) and modulators of (II) are useful for
CC prophylaxis or treatment of one or more cancers. (II) is also useful for
CC creating transgenic animals useful for studying the in vivo activities of
CC the polypeptide as well as for studying modulators of the polypeptides.
CC (I) induces the proliferation of neural cells and regeneration of nerve
CC and brain tissue and is useful for the treatment of central and
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral

CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,
 CC or periodontal disease. Furthermore, (I) is also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myaesthesia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention
 XX
 SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 4; Length 367;
 Best Local Similarity 94.3%; Pred. No. 2.5e-177;
 Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVKLLAKRKSDDGAF 60
 Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVKLLAKRKSDDGAF 60
 QY 61 YAVKVLQKKSILKKEQHMAERNVLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 120
 Db 61 YAVKVLQKKSILKKEQHMAERSVLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 120
 QY 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHSLNIIYRDLPENILLDCQGHVLTDFGL 180
 Db 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHSLNIIYRDLPENILLDCQGHVLTDFGL 180
 QY 181 CKECVEPETTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240
 Db 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDQVS 240
 QY 241 QMYENILHQPLOIPGGRVTAACDLQSLHKKQRLGSKEDFLDIKNHFFSPINWDDL 300
 Db 241 QMYENILHQPLOIPGGRVTAACDLQSLHKKQRLGSKEDFLDIKNHFFSPINWDDL 300
 QY 301 YHKRLTPPNPNVVEGPADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
 Db 301 YHKRLTPPNPNVVTGPADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
 QY 361 DDILD 366
 Db 361 DDILD 366

RESULT 5

AAE22765

ID AAE22765 standard; protein; 367 AA.

AC AAE22765;

XX AAE22765;

DT 09-AUG-2002 (first entry)

XX Human serum and glucocorticoid-induced protein kinase, SGK2-alpha.
 DE Human; cytostatic; antisense gene therapy; screening; protein kinase;
 KW cancer; liver; colon; tumour; inflammation; arthritic synovium; enzyme;
 KW serum and glucocorticoid-induced protein kinase; SGK2-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200224947-A2.

XX 28-MAR-2002.
 PD 20-SEP-2001; 2001WO-IB002237.
 XX 20-SEP-2000; 2000US-0233999P.
 PF 02-OCT-2000; 2000US-0237419P.
 XX 02-OCT-2000; 2000US-0237423P.
 PR 04-OCT-2000; 2000US-023858P.
 PR 10-MAY-2001; 2001US-0290555P.
 XX (KINE-) KINETEK PHARM INC.
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX Yoganathan T, Delaney AD;
 PI WPI; 2002-394145/42.
 XX N-PSDB; AAD36141.
 DR Diagnosing cancer, comprises determining the upregulation of expression
 XX of a nucleic acid sequence encoding a protein kinase or upregulation of
 PT expression of the protein kinase, in the cancer.
 PT
 XX Claim 1; Page 66-67; 87pp; English.
 XX
 CC The invention relates to a method for screening biologically active agent
 CC that modulates cancer associated protein kinase function. The invention
 CC also relates to a method for diagnosing cancer comprising determining the
 CC upregulation of expression of a nucleic acid sequence encoding a protein
 CC kinase. The method is useful for diagnosing cancer. A protein kinase is
 CC useful for screening biological agents that modulate cancer associated
 CC protein kinase function. Downregulating the activity of protein kinase is
 CC useful for inhibiting the growth of a cancer cell, e.g. liver or colon
 CC cancer. A nucleic acid encoding protein kinase is useful to screen biopsy
 CC derived tumours and inflammatory samples such as arthritic synovium, for
 CC amplified DNA in the cell or increased expression of corresponding mRNA
 CC or protein and is also useful to detect differences in expression levels
 CC such as molecular weight, amino acid and nucleotide sequences between the
 CC two cells. The present sequence is human serum and glucocorticoid-induced
 CC protein kinase, SGK2-alpha
 XX
 SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 5; Length 367;
 Best Local Similarity 94.3%; Pred. No. 2.5e-177;
 Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MASSPVGVPSQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVKLLAKRKSDDGAF 60
 Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVKLLAKRKSDDGAF 60
 QY 61 YAVKVLQKKSILKKEQHMAERNVLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 120
 Db 61 YAVKVLQKKSILKKEQHMAERSVLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 120
 QY 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHSLNIIYRDLPENILLDCQGHVLTDFGL 180
 Db 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHSLNIIYRDLPENILLDCQGHVLTDFGL 180
 QY 181 CKECVEPETTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240
 Db 181 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMLHGLPPFYSDQVS 240
 QY 241 QMYENILHQPLOIPGGRVTAACDLQSLHKKQRLGSKEDFLDIKNHFFSPINWDDL 300
 Db 241 QMYENILHQPLOIPGGRVTAACDLQSLHKKQRLGSKEDFLDIKNHFFSPINWDDL 300
 QY 301 YHKRLTPPNPNVVEGPADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
 Db 301 YHKRLTPPNPNVVTGPADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
 QY 361 DDILD 366
 Db 361 DDILD 366

Db 361 DDDILD 366

RESULT 6
ADD45799
ID ADD45799 standard; protein; 367 AA.
XX
AC ADD45799;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein XP_009494, SEQ ID NO 11468.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-NOV-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; XP_009494.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Pegé; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 7; Length 367;

Best Local Similarity 94.3%; Pred. No. 2.5e-177;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGPSPPSRANGNINLGPSANPNARPTDFDLKVIKGNKGVLLAKRKSDGAF 60
DB 1 MNSSPAGTSPGPSRANGNINLGPSANPNARPTDFDLKVIKGNKGVLLAKRKSDGAF 60
QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 120
DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 120
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLEPRARFYAAEVASAIYGLHSLNIIYRDLKPNILLDCQGHVLTDFGL 180
QY 181 CKECVEPEETSTFCGTPEVLAPEVLRKEPYDRAVDWMCILGAVLYEMLHGLPPEFNTDVA 240
DB 181 CKEGVEPEETSTFCGTPEVLAPEVLRKEPYDRAVDWMCILGAVLYEMLHGLPPEFNTDVA 240
QY 241 QMYENILHQPLOIPGGRITVAACDQLLQGLLHKDQRLGSKEDFLDKNHHFFSPINWDDL 300
DB 241 QMYENILHQPLOIPGGRITVAACDQLLQGLLHKDQRLGSKADFLKIHVFFSPINWDDL 300
QY 301 YHKRLTPPNVNEGPAHLKHFDEPTQBAVSKSIGCTPDTVASSGASSAFGLGFSYAQD 360
DB 301 YHKRLTPPNVNEGPAHLKHFDEPTQBAVSKSIGCTPDTVASSGASSAFGLGFSYAQD 360
QY 361 DDDILD 366
DB 361 DDDILD 366

RESULT 7
ADI29317
ID ADI29317 standard; protein; 367 AA.
XX
AC ADI29317;
XX
DT 22-APR-2004 (first entry)
XX
DE Human MARK3-associated protein #87.
XX
KW Human; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorder;
KW hyperproliferative disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003232771-A1.
XX
PD 18-DEC-2003.
XX
PF 17-JUN-2002; 2002US-00174319.
XX
PR 17-JUN-2002; 2002US-00174319.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Freier SM, Dobie KW;
XX
DR WPI; 2004-052188/05.
DR N-PSDB; ADI29435.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
PT expression of MARK3 or for treating cancer or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 237; 233pp; English.
XX
CC The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding MARK3
CC (MAP/microtubule affinity-regulating kinase 3), that specifically

CC hybridises with the nucleic acid encoding MARK3 and inhibits expression
CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
CC composition comprising the compound and a carrier or diluent, inhibiting
CC the expression of MARK3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with MARK3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer and neurodegenerative diseases e.g.
CC Alzheimer's disease. The present sequence is a MARK3 associated protein
CC included in the figures but not mentioned anywhere else in the
CC specification.
XX
SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 8; Length 367;
Best Local Similarity 94.3%; Pred. No. 2.5e-177;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKS DGAF 60
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db 61 YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
QY 181 KCEGVEPEETTTSTFCGTPEYLAPEVLKRPYDRAVDMWCLGAVLYEMLHGLPPFTNDVA 240
Db 181 KCEGVEPEETTTSTFCGTPEYLAPEVLKRPYDRAVDMWCLGAVLYEMLHGLPPFTNDVA 240
QY 241 QMYENILHQLQIPGGRTVAACDLQLLHKDQORQLGSKEDFLDIKNHMFSPINWDDL 300
Db 241 QMYENILHQLQIPGGRTVAACDLQLLHKDQORQLGSKADFLDIKNHVFSPINWDDL 300
QY 301 YHKRLTPFPNPNVEGPADLKHDFPFTQBAVSKSIGCTPDTVASSSGASSAFGLGFSYAQD 360
Db 301 YHKRLTPFPNPNVTGPADLKHDFPFTQBAVSKSIGCTPDTVASSSGASSAFGLGFSYAPE 360
QY 361 DDDILD 366
Db 361 DDDILD 366

RESULT 8
ID ADJ45521 standard; protein; 367 AA.
XX
AC ADJ45521;
XX
DT 06-MAY-2004 (first entry)
XX
DE LXR-ligand induced transcript seq id 52.
XX
KW LXR; liver X receptor; cholesterol; gallstone; atherosclerosis;
KW lipid storage disease; obesity; diabetes; hypercholesterolaemia;
KW LXR-ligand induced 1; LXR1; human; LXR-ligand induced transcript;
KW LXR regulated gene.
XX
OS Homo sapiens.
XX
PN US2004023276-A1.
XX
PD 05-FEB-2004.
XX
PF 02-MAY-2003; 2003US-00429160.
XX
PR 03-MAY-2002; 2002US-0377714P.
XX
PA (WARD/) WARD T R.

PA (MAOM/) MAO M.
PA (LINS/) LINSLEY P S.
PA (LUND/) LUND E.
XX
XX Ward TR, Mao M, Linsley PS, Lund E;
PI WPI; 2004-224687/21.
DR N-PSDB; ADJ45520.
XX
PT New purified liver X receptor (LXR) nucleic acids, useful for diagnosing
PT a disease involving LXR activity, such as cholesterol gallstones,
PT atherosclerosis, lipid storage diseases, obesity, diabetes, or
PT hypercholesterolemia.
XX
XX Example 1; SEQ ID NO 52; 141pp; English.
XX
CC The invention describes a purified nucleic acid comprising a fully
CC defined sequence of 1586 bp (SEQ ID NO: 1) as given in the specification,
CC or its complement. The methods and compositions are useful for diagnosing
CC a disease or disorder involving LXR (liver X receptor) activity in a
CC sample by detecting an increase or decrease in the transcript level
CC relative to the amount present in an analogous sample from a subject not
CC having the disease or disorder or not subjected to therapy, wherein the
CC disease or disorder is cholesterol gallstones, atherosclerosis, lipid
CC storage diseases, obesity, diabetes, or hypercholesterolaemia. They are
CC also used to identify a compound that changes LXR activity, wherein the
CC compound changes the estimated level of LXR activity in a sample from the
CC subject contacted with the compound relative to the estimated level of
CC LXR activity in an analogous sample from the subject not contacted with
CC the compound. This is the amino acid sequence of an LXR regulated
CC protein.
XX
SQ Sequence 367 AA;

Query Match 94.3%; Score 1848; DB 8; Length 367;
Best Local Similarity 94.3%; Pred. No. 2.5e-177;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKS DGAF 60
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNYGKVLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db 61 YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
Db 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
QY 181 KCEGVEPEETTTSTFCGTPEYLAPEVLKRPYDRAVDMWCLGAVLYEMLHGLPPFTNDVA 240
Db 181 KCEGVEPEETTTSTFCGTPEYLAPEVLKRPYDRAVDMWCLGAVLYEMLHGLPPFTNDVA 240
QY 241 QMYENILHQLQIPGGRTVAACDLQLLHKDQORQLGSKEDFLDIKNHMFSPINWDDL 300
Db 241 QMYENILHQLQIPGGRTVAACDLQLLHKDQORQLGSKADFLDIKNHVFSPINWDDL 300
QY 301 YHKRLTPFPNPNVEGPADLKHDFPFTQBAVSKSIGCTPDTVASSSGASSAFGLGFSYAQD 360
Db 301 YHKRLTPFPNPNVTGPADLKHDFPFTQBAVSKSIGCTPDTVASSSGASSAFGLGFSYAPE 360
QY 361 DDDILD 366
Db 361 DDDILD 366
RESULT 9
ID AAM25594 standard; protein; 382 AA.
XX
AC AAM25594;
XX

DT	16-OCT-2001	(first entry)	
DE	Human protein sequence SEQ ID NO:1109.		
XX	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;		
KW	antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;		
KW	antibacterial; endocrine; cardiant; central nervous system; virucide;		
KW	anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;		
KW	antiaggregant; haemostatic; vulnerary; antilucer; osteopathic; eczema;		
KW	dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;		
KW	neuroprotective; antidepressant; neurotropic; antiparkinsonian; infection;		
KW	immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;		
KW	antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;		
KW	cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;		
KW	genetic disease; haematopoietic disorder; platelet disorder; asthma;		
KW	thrombocytopaenia; osteoporosis; severe combined immunodeficiency;		
KW	allergic rhinitis; diabetes; multiple sclerosis; depression;		
KW	Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;		
XX	neurological disorder.		
OS	Homo sapiens.		
XX	WO200153455-A2.		
PN	26-JUL-2001.		
XX	22-DEC-2000; 2000WO-US035017.		
PF	23-DEC-1999; 99US-00471275.		
XX	21-JAN-2000; 2000US-00488725.		
PR	25-APR-2000; 2000US-00552317.		
XX	(HYSE-) HYSEQ INC.		
PA	Tang YT, Liu C, Drmanac RT;		
XX	WPI; 2001-457603/49.		
PI	N-PSDB; AAH99535.		
XX	Isolated human polynucleotides encoding polypeptides, useful for the		
PT	treatment and diagnosis of e.g. cancer, ulcers and HIV infection.		
XX	Claim 20; Page 227; 1217pp; English.		
PS	AAH99166 to AAH99904 encode the human proteins given in AAM25225 to		
XX	AAM25963. The proteins can have activities based on the tissues and cells		
CC	they are expressed in, such as: antiinflammatory; antirheumatic;		
CC	antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;		
CC	central nervous system; virucide; anti-HIV; fungicide; antimutagen;		
CC	cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;		
CC	antilucer; osteopathic; dermatological; antiallergic; antiasthmatic;		
CC	antidiabetic; cytostatic; neuroprotective; antidepressant; neurotropic;		
CC	antiparkinsonian; and immunostimulant. The proteins and polynucleotides		
CC	encoding them can be used in gene therapy, antisense therapy and vaccine		
CC	production. The proteins and polynucleotides are useful for screening for		
CC	agonists or antagonists of a protein and for the treatment and diagnosis		
CC	of disorders associated with the activity of a protein e.g. inflammation,		
CC	rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,		
CC	neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal		
CC	infections, autoimmunity, genetic diseases, haematopoietic disorders,		
CC	anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,		
CC	osteoporosis, severe combined immunodeficiency, eczema, allergic		
CC	rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression.		
CC	Alzheimer's disease, Parkinson's disease, neurodegenerative and		
CC	neurological disorders		
XX	Sequence 382 AA;		
SQ	Query Match 94.3%; Score 1848; DB 4; Length 382;		
	Best Local Similarity 94.3%; Pred. No. 2.6e-177;		
	Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;		
QY	1 MASSPVGVPSPPSPRANGNINLPSANPNARPTDFDLKVGKNGYKVLAKRKS DGAF 60		

Db	16	MNSSPAGTSPQPSRANGNINLGSANPNQAQPTDFDLKVGKNGYKVLAKRKS	DGAF	75		
Qy	61	YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPFLVGLRYSFQTP	PEKLYFVL	DYVNGGE 120		
Db	76	YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPFLVGLRYSFQTP	PEKLYFVL	DYVNGGE 135		
Qy	121	LFFHLQRRERFLPRARFYTAEVASAI	GYLHSLNIIYRDLK	KPENILLDCQGHVVL	TD	FGL 180
Db	136	LFFHLQRRERFLPRARFYAAEVASAI	GYLHSLNIIYRDLK	KPENILLDCQGHVVL	TD	FGL 195
Qy	181	CKEVEPEETSTFCGTP	PEYLAPEVL	RKEPYRDAVDMWCLGAVLYEMLHGL	PP	FTDVA 240
Db	196	CKEVEPEEDTSTFCGTP	PEYLAPEVL	RKEPYRDAVDMWCLGAVLYEMLHGL	PP	FYSQDVS 255
Qy	241	QWYENILHQPLQIPGGR	TVAACDLQLGLLHKDQORQLGSKEDFLDIKNHMF	FSPINWDDL	300	
Db	256	QWYENILHQPLQIPGGR	TVAACDLQLGLLHKDQORQLGSKADFLFIKNHVF	FSPINWDDL	315	
Qy	301	YHKRLTPFPNPNVVEG	PADLKHFPDFTQEA	VSKSIGCTPTDVASSSGASSA	FLGFSYAQD	360
Db	316	YHKRLTPFPNPNVTG	PADLKHFPDFTQEA	VSKSIGCTPTDVASSSGASSA	FLGFSYAPE	375
Qy	361	DDILD	366			
Db	376	DDILD	381			
RESULT 10						
ADY37607						
ID	ADY37607 standard; protein; 396 AA.					
XX	ADY37607;					
XX	ADY37607;					
DT	19-MAY-2005 (first entry)					
XX	Lung cancer related protein, SEQ ID 83.					
DE	Cytostatic; lung tumor.					
KW	Homo sapiens.					
OS	US2005048589-A1.					
PN	03-MAR-2005.					
PD	25-AUG-2004; 2004US-00926543.					
PF	25-AUG-2003; 2003US-0497790P.					
PR	(JEND/) JENDOUBI M.					
XX	Jendoubi M;					
PI	WPI; 2005-221517/23.					
XX	N-PSDB; ADY37561.					
DR	New antibody specific for an antigen differentially expressed between					
PT	lung cancer tissue and normal tissue, useful for diagnosing, treating or					
PT	preventing lung cancer.					
XX	Disclosure; SEQ ID NO 83; 171pp; English.					
PS	The present invention relates to an antibody (I) that binds to an antigen					
XX	that is differentially expressed between lung cancer tissue and normal					
CC	tissue, where the antigen is encoded by ADY37525. Also disclosed are					
CC	polypeptides (ADY37573-ADY37618) encoded by lung cancer related genes					
CC	(ADY37525-ADY37572), their fragments, analogs or derivatives; producing					
CC	lung cancer related polypeptides; and a diagnostic kit for detection and					
CC	disease management of lung cancer. (I) is useful for characterizing and					
CC	analyzing biological activity and function of the lung cancer-specific					
CC	gene products in relation to cellular pathways and networks in normal and					
CC	disease states, purifying the cancer specific gene products, and					

CC detecting lung cancer-specific gene products and their expression levels
CC in animal models of cancer. (I) is also useful for diagnosing, treating
CC or preventing lung cancer, and also disorders related to abnormal
CC cellular differentiation, proliferation or degeneration.

XX SQ Sequence 396 AA;

Query Match 94.3%; Score 1848; DB 9; Length 396;
Best Local Similarity 94.3%; Pred. No. 2.8e-177;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVPSQPSRANGINILGPSANPNARPTDFELKVIKGNVGVLLAKRKSQDGAF 60
DB 30 MNSSPAGTSPQPSRANGINILGPSANPNARPTDFELKVIKGNVGVLLAKRKSQDGAF 89
QY 61 YAVKVLQKKSILKKEQSHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
DB 90 YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 149
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHSLNIIYRDLKBPENILLDCQGHVLTDFGL 180
DB 150 LFFHLQRRERFLEPRARFYAAEVAESAIGYLHSLNIIYRDLKBPENILLDCQGHVLTDFGL 209
QY 181 CKCEVEPEETSTFCGTPPEYLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFNTDVA 240
DB 210 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFSQDVS 269
QY 241 QMYENILHQPLOIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
DB 270 QMYENILHQPLOIPGGRTVAACDLQLGLLHKDQRLGSKADFLKHNHVFSPINWDDL 329
QY 301 YHKRLTPPNPNVEGPADLKHDFDPEFTQBAVSKSIGCTPDTVASSSGASSAFGLGFSYAQD 360
DB 330 YHKRLTPPNPNVTGPADLKHDFDPEFTQBAVSKSIGCTPDTVASSSGASSAFGLGFSYAPE 389
QY 361 DDDILD 366
DB 390 DDDILD 395

RESULT 11
AAY95276
ID AAY95276 standard; protein; 427 AA.
XX AC AAY95276;
XX DT 12-SEP-2000 (first entry)
XX DE Human serum and glucocorticoid-induced protein kinase 2-beta.
XX KW Serum and glucocorticoid-induced protein kinase 2; SGK2-beta; human;
KW phosphorylation; cancer; diabetes; ischaemia; therapy.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Modified-site 339 /note= "O-phosphorylated"
FT Modified-site 394 /note= "O-phosphorylated"
XX WO200035946-A1.
XX PD 22-JUN-2000.
XX PF 14-DEC-1999; 99WO-GB004232.
XX PR 14-DEC-1998; 98US-0112217P.
XX PR 19-AUG-1999; 99GB-00019676.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Cohen P, Kobayashi T, Deak M;

XX WPI: 2000-442364/38.
DR N-PSDB; AAA27857.
XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)
PT or dephosphorylation, useful for treatment of cancer, diabetes and
PT ischemic diseases.
XX Disclosure; Page 6-7; 127pp; English.

XX The present sequence is that of human serum and glucocorticoid-induced
CC protein kinase (SGK) isoform 2-beta. SGK (see AAY95276) was initially
CC identified as a glucocorticoid and osmotic stress-responsive gene. Novel
CC isoforms, SGK2 and SGK3, were isolated from EST database searches, and 2
CC splice variants of SGK2, i.e. SGK2-beta and -alpha (see AAY95275), which
CC contains 60 fewer N-terminal residues, were identified. SGK2-beta is
CC expressed in liver and kidney. It is activated by phosphorylation in a
CC similar manner to SGK. The invention provides methods of activating SGK
CC activity by phosphorylation using 3-phosphoinositide-dependent protein
CC kinase-1 (PDK1), and of reducing the activity of SGK by
CC dephosphorylation. The invention also provides a method of identifying a
CC compound that modulates the activity of SGK. Such compounds are useful
CC for treating patients requiring modulation of SGK, such as patients with
CC cancer, diabetes or ischaemic disease

SQ Sequence 427 AA;

Query Match 94.3%; Score 1848; DB 3; Length 427;
Best Local Similarity 94.3%; Pred. No. 3.1e-177;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVPSQPSRANGINILGPSANPNARPTDFELKVIKGNVGVLLAKRKSQDGAF 60
DB 61 MNSSPAGTSPQPSRANGINILGPSANPNARPTDFELKVIKGNVGVLLAKRKSQDGAF 120
QY 61 YAVKVLQKKSILKKEQSHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
DB 121 YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 180
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHSLNIIYRDLKBPENILLDCQGHVLTDFGL 180
DB 181 LFFHLQRRERFLEPRARFYAAEVAESAIGYLHSLNIIYRDLKBPENILLDCQGHVLTDFGL 240
QY 181 CKCEVEPEETSTFCGTPPEYLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFNTDVA 240
DB 241 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFSQDVS 300
QY 241 QMYENILHQPLOIPGGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
DB 301 QMYENILHQPLOIPGGRTVAACDLQLGLLHKDQRLGSKADFLKHNHVFSPINWDDL 360
QY 301 YHKRLTPPNPNVEGPADLKHDFDPEFTQBAVSKSIGCTPDTVASSSGASSAFGLGFSYAQD 360
DB 361 YHKRLTPPNPNVTGPADLKHDFDPEFTQBAVSKSIGCTPDTVASSSGASSAFGLGFSYAPE 420
QY 361 DDDILD 366
DB 421 DDDILD 426

RESULT 12
ADQ88284
ID ADQ88284 standard; protein; 427 AA.
XX AC ADQ88284;
XX DT 21-OCT-2004 (first entry)
XX DE Human 54946 protein, a Ser/Thr protein kinase SGK2.
XX KW human; cardiovascular disorder; thrombotic disorder;
KW differential expression; gene therapy; aberrant vascularisation;

KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;
 KW dyslipidaemia; high blood pressure; heart failure; cardiomyopathy;
 KW thrombolytic; anticoagulant; antilipemic; hypotensive; cardiant;
 KW Ser/Thr protein kinase; SGK2; EC 2.7.1.37; enzyme.

OS Homo sapiens.

XX WO2004063340-A2.

XX 29-JUL-2004.

XX 13-JAN-2004; 2004WO-US000393.

XX 13-JAN-2003; 2003US-0439693P.

XX 05-FEB-2003; 2003US-0445216P.

XX 18-FEB-2003; 2003US-0448036P.

XX 12-MAR-2003; 2003US-0454189P.

XX 25-MAR-2003; 2003US-0457541P.

XX 23-APR-2003; 2003US-0466411P.

XX 08-MAY-2003; 2003US-0469041P.

XX 10-JUN-2003; 2003US-0477414P.

XX 13-JUN-2003; 2003US-0478560P.

XX 24-JUL-2003; 2003US-0489772P.

XX 28-JUL-2003; 2003US-0490660P.

XX 03-SEP-2003; 2003US-0499838P.

XX 22-SEP-2003; 2003US-0504786P.

XX 24-SEP-2003; 2003US-0505570P.

XX 17-OCT-2003; 2003US-0512418P.

XX 27-OCT-2003; 2003US-0514660P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;

XX Rogrigue-Way A, Tomlinson JB;

XX WPI; 2004-553729/53.

XX N-PSDB; ADQ88283.

XX Identifying a compound for treating a cardiovascular or thrombotic

XX disorder by combining a compound to be tested with e.g., a 9380, 9462,

XX 8701 or 2419 polypeptide or with a host cell expressing the polypeptide

XX and detecting the binding.

XX Claim 1; SEQ ID NO 126; 512pp; English.

XX This invention relates to a novel compound that is capable of treating a

XX cardiovascular or thrombotic disorder. Specifically, it refers to the

XX identification of nucleic acid molecules, and the encoded proteins

XX thereof, which are differentially expressed in cardiovascular disease

XX states relative to their normal expression in non-diseased tissues. The

XX present invention describes test compounds (i.e. small molecules,

XX peptides or antibodies) that can bind to and modulate the activity of

CC Query Match 94.3%; Score 1848; DB 8; Length 427;
 CC Best Local Similarity 94.3%; Pred. No. 3.1e-177;
 CC Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGINILGPSANPNARPTDFDLKVGKNGYGVLLAKRKSDDGAF 60

DB 61 MNSSPAGTSPQPSRANGINILGPSANPNARPTDFDLKVGKNGYGVLLAKRKSDDGAF 120

QY 61 YAVKVLQKKSILKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 120
 DB 121 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGE 180
 QY 121 LFFHLQRRRFLPRARFYTAEVASAIYGLHLSNIIYRDLKPNILLDCQGHVVLDTFGL 180
 DB 181 LFFHLQRRRFLPRARFYAAEVASAIYGLHLSNIIYRDLKPNILLDCQGHVVLDTFGL 240
 QY 181 CKECVPEETTSFCTGTPYLAPVLRKPYDRAVDMWCLGAVLYEMLHGLPPFNTDVA 240
 DB 241 CKEGVPEETTSFCTGTPYLAPVLRKPYDRAVDMWCLGAVLYEMLHGLPPFNSQDVS 300
 QY 241 QMYENILHQPLOIPIGGRITVAACDLQLLHKDQORQLSGKEDFLDKNHNFFSPINWDDL 300
 DB 301 QMYENILHQPLOIPIGGRITVAACDLQLLHKDQORQLSGKADFLKHNHFFSPINWDDL 360
 QY 301 YHKRLTPFPNPNVGGPADLKHDPFTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAQD 360
 DB 361 YHKRLTPFPNPNVGTGADLKHDPFTQBAVSKSIGCTPDTVASSSGASSAFILGFSYAPE 420
 QY 361 DDDILD 366
 DB 421 DDDILD 426

RESULT 13

AAB65708

ID AAB65708 standard; protein; 367 AA.

XX AAB65708;

XX 27-MAR-2001 (first entry)

XX Novel protein kinase, SEQ ID NO: 237.

XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.

OS Homo sapiens.

XX WO2000073469-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014842.

XX 28-MAY-1999; 99US-0136503P.

XX (SUGB-) SUGEN INC.

XX Plowman GD, Martinez R, Whyte D, Sudersanam S;

XX WPI: 2001-032161/04.

XX N-PSDB; AAP44737.

XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.

XX Claim 10; Fig 1; 310pp; English.

XX The present sequence is a novel protein kinase. The novel protein kinases
 CC and the nucleic acids that encode them may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies

CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX
SQ Sequence 367 AA;
Query Match 94.2%; Score 1846; DB 4; Length 367;
Best Local Similarity 94.0%; Pred. No. 3.9e-177;
Matches 344; Conservative 11; Mismatches 11; Indels 0; Gaps 0;
QY 1 MASSPVGVSPQPSRANGINILGPSANPNARPTDFDLKVIKGNYGKVLAKRKSDDGAF 60
DB 1 MNSSPAGTSPQPSRANGINILGPSANPNARPTDFDLKVIKGNYGKVLAKRKSDDGAF 60
QY 61 YAVKVLQKKSILKNKEQHIMAEARNVLLKNVRHPLVGLRYSFQPEKLYFVLDDYVNGGE 120
DB 61 YAVKVLQKKSILKKKEQHIMAEARNVLLKNVRHPLVGLRYSFQPEKLYFVLDDYVNGGE 120
QY 121 LFFHLQRRERFLEPRAREVTAFAVSAIGVLSHINIIYLDLKPENILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLEPRAREVTAFAVSAIGVLSHINIIYLDLKPENILLDCQGHVLTDFGL 180
QY 181 CREKVEPETTTFTCTPEYLAPEVLVRKEPPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240
DB 181 CREKVEPETTTFTCTPEYLAPEVLVRKEPPYDRAVDWVCLGAVLYEMLHGLPPFFSQDVS 240
QY 241 QMYENILHQLPIPGRTVAACDLQLGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 300
DB 241 QMYENILHQLPIPGRTVAACDLQLGLLHKDQRLGSKADFLDIKNHFFSPINWDDL 300
QY 301 YHKRLTPPNVNGPADLKHDPDPTQEAVSKSGCTPDTVASSSGASSAFLGESYAQD 360
DB 301 YHKRLTPPNVNGPADLKHDPDPTQEAVSKSGCTPDTVASSSGASSAFLGESYAPE 360
QY 361 DDDILD 366
DB 361 DDDILD 366

RESULT 14
ADA05780
ID ADA05780 standard; protein; 398 AA.
AC ADA05780;
XX
XX 06-NOV-2003 (first entry)
XX Human NOV33a protein SEQ ID NO:140.
XX human; NOV3; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
XX
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 12-OCT-2001; 2001US-0328056P.
PR 15-OCT-2001; 2001US-0328849P.
PR 17-OCT-2001; 2001US-0329414P.
PR 18-OCT-2001; 2001US-0330142P.
PR 22-OCT-2001; 2001US-0330309P.
PR 24-OCT-2001; 2001US-0332666P.
PR 24-OCT-2001; 2001US-0332629P.
PR 29-OCT-2001; 2001US-0343629P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Pattarajan M, Szytek KA, Edinger SR, Ellerman K, Malyankar UM; B;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkens RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05779.
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 1; Page 219; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity of or latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic

CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, hematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.

XX SQ Sequence 398 AA;

Query Match 85.5%; Score 1674.5; DB 6; Length 398;
Best Local Similarity 86.9%; Pred. No. 9.1e-160;
Matches 318; Conservative 9; Mismatches 10; Indels 29; Gaps 1;
QY 1 MASSPVGPSPQSRANGINILGFSANPNARPTDFDLKVGKNGYKVLAKRKSDGAF 60
DB 61 MNSSPAGTSPQSRANGINILGFSANPNARPTDFDLKVGKNGYKVLAKRKSDGAF 120
QY 61 YAVKVLQKKSILKNKEQHIMARNVLLKNVRHFLVGLRYSFQTPEKLYFVLDYVNGGE 120
DB 121 YAVKVLQKKSILKNKEQHIMARNVLLKNVRHFLVGLRYSFQTPEKLYFVLDYVNGGE 180
QY 121 LFFHLQRRERFLPRARFYTAEVASAIYGLHSLNIYRDLKPNILLDCQGHVLTDFGL 180
DB 181 LFFHLQRRERFLPRARFYTAEVASAIYGLHSLNIYRDLKPNILLDCQ----- 230
QY 181 CKECVPEETTSFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPFFNTDVA 240
DB 231 -----YLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPFFYSDVS 271
QY 241 QMYENILHQLQIPGGRVAAACDLQGLLHKQRLGSKEDFLDKNHMFFSPINWDDL 300
DB 272 QMYENILHQLQIPGGRVAAACDLQGLLHKQRLGSKADFLKKNHFFSPINWDDL 331
QY 301 YHKRLTPPNPNVEGADLKHFPDFTQEAIVSKSIGCTPDTVASSGASSAFILGFSYAQD 360
DB 332 YHKRLTPPNPNVTGPADLKHFPDFTQEAIVSKSIGCTPDTVASSGASSAFILGFSYAPE 391
QY 361 DDDILD 366
DB 392 DDDILD 397

RESULT 15

ADN62944

ID ADN62944 standard; protein; 398 AA.

XX AC ADN62944;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV33a.

XX human; NOVX;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW hematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

XX PD 26-FEB-2004.

XX PF 01-OCT-2002; 2002US-00262511.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 29-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 22-APR-2002; 2002US-0373884P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381042P.
PR 28-MAY-2002; 2002US-0381642P.
PR 29-MAY-2002; 2002US-0383656P.
PR 25-JUN-2002; 2002US-0383831P.
XX XX

(SMIT/) SMITHSON G.

(MILL/) MILLET I.

(PEYM/) PEYMAN J A.

(KEKU/) KEKUDA R.

(JUUG/) JU J.

(LILL/) LI L.

(GUOX/) GUO X.

(PATT/) PATTURAJAN M.

(SPYT/) SPYTEK K A.

(EDIN/) EDINGER S R.

(ELLE/) ELLERMAN K.

(MALY/) MALYANKAR U M.

(ORTT/) ORT T.

(GORM/) GORMAN L.

(ZERH/) ZERHUSEN B D.

(ANDE/) ANDERSON D W.

(ZHON/) ZHONG M.

(CATT/) CATTERTON E.

(JIWW/) JI W.

(MILL/) MILLER C B.

(RAST/) RASTELLI L.

(STON/) STONE D J.

(PENA/) PENA C E A.

(SHEN/) SHENOY S G.

(SHIM/) SHIMKETS R A.

(ROTH/) ROTHENBERG M E.

(LEAC/) LEACH M D.

(AGER/) AGEE M L.

(BERG/) BERGHS C.

(DIPI/) DIPPO V A.

(EISE/) EISEN A.

(GANG/) GANGOLLI B A.

(RIEG/) RIEGER D K.

(SPAD/) SPADERNA S K.

XX XX

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;

PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;

PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI: 2004-213931/20.

DR N-PSDB; ADN62943.

XX XX

PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,

XX diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:21:11 ; Search time 17.3113 Seconds
(without alignments)
1752.724 Million cell updates/sec

Title: US-09-868-131A-3

Perfect score: 1959

Sequence: 1 MASSPVGVPSQPSPRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfilese1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	70.8	407	2	US-10-067-977-4
2	1387	70.8	445	2	US-10-067-977-2
3	1383	70.6	431	2	US-09-031-295-2
4	1383	70.6	431	2	US-10-000-039-2
5	1380.5	70.5	430	1	US-08-712-709-9
6	1380.5	70.5	430	2	US-09-111-444-9
7	1380.5	70.5	430	2	US-09-541-228-9
8	1379	70.4	431	1	US-08-712-709-5
9	1379	70.4	431	2	US-09-111-444-5
10	1379	70.4	431	2	US-09-541-228-5
11	863	44.1	479	2	US-09-771-161A-246
12	863	44.1	479	2	US-09-771-161A-247
13	863	44.1	479	2	US-09-771-161A-248
14	860	43.9	465	2	US-09-526-043-2
15	858	43.8	454	2	US-09-526-043-17
16	851.5	43.5	480	2	US-09-590-740-6
17	851	43.4	480	2	US-09-526-043-13
18	851	43.4	481	2	US-09-538-092-1054
19	847.5	43.3	480	2	US-09-091-058-2
20	847.5	43.3	480	2	US-09-590-740-2
21	847.5	43.3	480	2	US-09-538-092-1053
22	847.5	43.3	480	2	US-09-526-043-14
23	847.5	43.3	480	2	US-09-771-161A-223
24	847.5	43.3	726	2	US-09-417-197-71
25	847.5	43.3	727	2	US-09-417-197-139
26	831.5	42.4	470	2	US-09-248-796A-18482
27	829	42.3	417	2	US-09-590-740-4

28	822.5	42.0	480	2	US-09-205-658-157	Sequence 157, App
29	794.5	40.6	482	2	US-09-430-564-2	Sequence 2, Appli
30	794.5	40.6	495	2	US-09-430-564-3	Sequence 3, Appli
31	794.5	40.6	495	2	US-09-762-258-2	Sequence 2, Appli
32	792	40.4	637	2	US-09-817-310-2	Sequence 2, Appli
33	792	40.4	637	2	US-10-355-724A-2	Sequence 2, Appli
34	780.5	39.8	502	1	US-09-538-092-996	Sequence 996, App
35	780.5	39.8	525	1	US-08-749-902-7	Sequence 7, Appli
36	780.5	39.8	525	1	US-08-749-902-8	Sequence 8, Appli
37	780.5	39.8	525	2	US-09-430-564-16	Sequence 16, Appli
38	780.5	39.8	525	2	US-09-762-258-4	Sequence 4, Appli
39	778.5	39.7	587	1	US-08-313-274-2	Sequence 2, Appli
40	778.5	39.7	655	2	US-09-949-016-11676	Sequence 11676, A
41	777.5	39.7	546	2	US-09-205-658-155	Sequence 155, App
42	773	39.5	541	2	US-09-205-658-154	Sequence 154, App
43	764	39.0	568	2	US-09-949-016-7970	Sequence 7970, Ap
44	764	39.0	584	2	US-09-842-307-2	Sequence 2, Appli
45	750	38.3	737	2	US-09-772-647-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-067-977-4

; Sequence 4, Application US/10067977

; Patent No. 6830911

; GENERAL INFORMATION:

; APPLICANT: YAN, Chunhua and KE, Zhaoxi

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CL001313

; CURRENT APPLICATION NUMBER: US/10/067,977

; CURRENT FILING DATE: 2002-02-08

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 407

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-067-977-4

Query Match	70.8%;	Score 1387;	DB 2;	Length 407;
Best Local Similarity	71.1%;	Pred. No. 8.8e-127;		
Matches	256;	Conservative 51;	Mismatches 49;	Indels 4; Gaps 2;
QY	9	PSQPSPRANGNINLSPSNAPNAPPTDFELKVIKGNYGKVLAKRSGDGFYAVKVLQK	68	
Db	49	PSPPSPSQ-QINLGPSSNPHAKPSDFELKVIKGSFGKVLARHKAEEVFYAVKVLQK	107	
QY	69	KSILKKEQNHMAERNVLLKNVRHFFLVGLRYSFOTPEKLYPVLGYVNGGELFFHLORE	128	
Db	108	KAILKKKEKHIMSERNVLLKNVGHFVLGLHFSFQTADKLYPVLGYINGELFFHLORE	167	
QY	129	RFLEPRARFYAEVASAIGYLHSLNIIVRDLPENILLDCQGHVLTDFGLCKECVEPE	188	
Db	168	RCFLEPRARFYAEATASALCYLHSLNIVRDLPENILLDSQSHIVLTDFGLCKENIEHN	227	
QY	189	ETTSTFCGTPPEYLAPVLKEPYDRAVDWVWCLGAVLYEMLHGLPPFPNTDVAQMYENILH	248	
Db	228	STTSTFCGTPPEYLAPVLKHQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNILN	287	
QY	249	QLOLPGGRTVAACDQLLOGLLHKDQRORIGSKEDFLDINKHMPFSPINWDDLXHKRLTTPP	308	
Db	288	KFLQLKPNITNSARHLLEGLOKRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITTPP	347	
QY	309	FNPVVEGPDALKHDFEFTQEAHSVKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL	365	
Db	348	FNPVSGPNDLRHDFEFTPEEPVPSIGKSPSVLVTASVKEAAEAFLGFSYAPPTDTSFL	407	

RESULT 2

APPLICATION NUMBER: US/09/031.295
FILING DATE: 26-FEB-1998
APPLICATION NUMBER: DE 197-08-173.8
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31.298
REFERENCE/DOCKET NUMBER: 058315/0123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-000-039-2

Query Match 70.6%; Score 1383; DB 2; Length 431;
Best Local Similarity 70.8%; Pred. No. 2.3e-126;
Matches 255; Conservative 52; Mismatches 49; Indels 4; Gaps 2;
QY 9 PPSQPSRANGNINLGPANPNARPTDFLKVIGKGNVGVLLAKRSGDGAFAVAVKVLQK 68
DB 73 PPSPPSPSQ-QINLGPSSNPHAKPSDFHFLKVIGKSGFGVLLARHKAEEVFVAVKVLQK 131
QY 69 KSLTKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 128
DB 132 KAILKKKEKHIMSERVLLKNVHPFLVGLHFSFQADKLYFVLDYINGGELFFHLORE 191
QY 129 RRELEPRARYTAEVAASAIYGLHSLNIYRDLPENILLDCQGHVLTDFGLCKECVEPE 188
DB 192 RCELEPRARYTAEVAASAIYGLHSLNIYRDLPENILLDCQGHVLTDFGLCKENIEHN 251
QY 189 ETTSTFCGTPPEYLAPEVLKRPYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
DB 252 STTSTFCGTPPEYLAPEVLKRPYDRTVDWMCGLGAVLYEMLYGLPPFYSRNTAEWYDNLN 311
QY 249 QPLOIPGGRTVAACDLLOGLLHKQORLGSKEDFLDIKNHMFSPINWDDLYHKLTPP 308
DB 312 KPLQLKNTNSARHLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLINKKITTP 371
QY 309 FNPVNGPADLKHFDPEFTQEAHSVKSIGCTPTDV---ASSSGASSAFLGFSYAQDDDDIL 365
DB 372 FNPVSGPNELRHFDPEFTPEEPVNSIGKSPDSVLVTASVKAAEAFLGFSYAPPTDSDL 431

RESULT 5
US-08-712-709-9
Sequence 9, Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709

FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-08-712-709-9
Query Match 70.5%; Score 1380.5; DB 1; Length 430;
Best Local Similarity 71.1%; Pred. No. 4.1e-126;
Matches 256; Conservative 53; Mismatches 46; Indels 5; Gaps 3;
QY 9 PPSQPSRANGNINLGPANPNARPTDFLKVIGKGNVGVLLAKRSGDGAFAVAVKVLQK 68
DB 73 PPSPPSPSQ-QINLGPSSNPHAKPSDFHFLKVIGKSGFGVLLARHKAEEVFVAVKVLQK 131
QY 69 KSLTKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 128
DB 132 KAILKKKEKHIMSERVLLKNVHPFLVGLHFSFQADKLYFVLDYINGGELFFHLORE 191
QY 129 RRELEPRARYTAEVAASAIYGLHSLNIYRDLPENILLDCQGHVLTDFGLCKECVEPE 188
DB 192 RCELEPRARYTAEVAASAIYGLHSLNIYRDLPENILLDCQGHVLTDFGLCKENIEHN 251
QY 189 ETTSTFCGTPPEYLAPEVLKRPYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
DB 252 GTTSTFCGTPPEYLAPEVLKRPYDRTVDWMCGLGAVLYEMLYGLPPFYSRNTAEWYDNLN 311
QY 249 QPLOIPGGRTVAACDLLOGLLHKQORLGSKEDFLDIKNHMFSPINWDDLYHKLTPP 308
DB 312 KPLQLK-NITNSARHLEGLLQKDRKRLGAKDDFMEIKSHIFSLINWDDLINKKITTP 370
QY 309 FNPVNGPADLKHFDPEFTQEAHSVKSIGCTPTDV---ASSSGASSAFLGFSYAQDDDDIL 365
DB 371 FNPVSGPSDLRHFDPEFTPEEPVPSIGRSPDSILVTASVKAAEAFLGFSYAPPMDSFL 430

RESULT 6
US-09-111-444-9
Sequence 9, Application US/09111444
Patent No. 6045792
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444

;/ FILING DATE:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/712,709
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Billings, Lucy J
;/ REGISTRATION NUMBER: 36,749
;/ REFERENCE/DOCKET NUMBER: PF-0118 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415-855-0555
;/ INFORMATION FOR SEQ ID NO: 9:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 430 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ IMMEDIATE SOURCE:
;/ LIBRARY: GenBank
;/ CLONE: 294637
;/ US-09-111-444-9

Query Match 70.5%; Score 1380.5; DB 2; Length 430;
Best Local Similarity 71.1%; Pred. No. 4.1e-126;
Matches 256; Conservative 53; Mismatches 46; Indels 5; Gaps 3;
QY 9 PSPQSRANGNINLGSANPNARPTDFDLKVIGKNGYKVLAKRKSDFAYAVKVLQK 68
Db 73 PSPPPSPQ-QINLGPSSNPHAKPSDFHLKVIGSGFGKVLARHKAEEAFYAVKVLQK 131
QY 69 KSILKNKEQHIMAERNVLLKNVRHPLVGLYSPQTPKLYFVLDYVNGGELFFHLORE 128
Db 132 KAILKKKEKHIMSERVLLKNVHPFLVGLHFSQTDKLYFVLDYINGGELFFHLORE 191
QY 129 RFLPRARFYAEVASAIGYLHSLNIIVRDLPENILLDCQGHVLTDFGLCKEVEPE 188
Db 192 RCFLEPRARFYAEIASALGYLHSLNIIVRDLPENILLDSQGHIVLTDFGLCKENIEHN 251
QY 189 ETTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
Db 252 GTTSTFCGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILN 311
QY 249 QPLQIPGGRTVAACDLQGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLHYKRLTTP 308
Db 312 KPLQLK-NITNSARHLEGLLQKRTKRLGAKDDFMEIKSHIFFSLLINWDDLINKKITPP 370
QY 309 FNPVSGPADLKHFDPEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365
Db 371 FNPVSGPSDLRHFDEFTPEEPVPSSIGRSPSILVTASVKEAAEAFLGFSYAPPMDSFL 430

RESULT 7
US-09-541-228-9
; Sequence 9, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

;/ SOFTWARE: FastSeq Version 1.5
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/541,228
;/ FILING DATE:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/712,709
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Billings, Lucy J
;/ REGISTRATION NUMBER: 36,749
;/ REFERENCE/DOCKET NUMBER: PF-0118 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415-855-0555
;/ TELEFAX: 415-845-4166
;/ INFORMATION FOR SEQ ID NO: 9:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 430 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ IMMEDIATE SOURCE:
;/ LIBRARY: GenBank
;/ CLONE: 294637
;/ US-09-541-228-9

Query Match 70.5%; Score 1380.5; DB 2; Length 430;
Best Local Similarity 71.1%; Pred. No. 4.1e-126;
Matches 256; Conservative 53; Mismatches 46; Indels 5; Gaps 3;
QY 9 PSPQSRANGNINLGSANPNARPTDFDLKVIGKNGYKVLAKRKSDFAYAVKVLQK 68
Db 73 PSPPPSPQ-QINLGPSSNPHAKPSDFHLKVIGSGFGKVLARHKAEEAFYAVKVLQK 131
QY 69 KSILKNKEQHIMAERNVLLKNVRHPLVGLYSPQTPKLYFVLDYVNGGELFFHLORE 128
Db 132 KAILKKKEKHIMSERVLLKNVHPFLVGLHFSQTDKLYFVLDYINGGELFFHLORE 191
QY 129 RFLPRARFYAEVASAIGYLHSLNIIVRDLPENILLDCQGHVLTDFGLCKEVEPE 188
Db 192 RCFLEPRARFYAEIASALGYLHSLNIIVRDLPENILLDSQGHIVLTDFGLCKENIEHN 251
QY 189 ETTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
Db 252 GTTSTFCGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILN 311
QY 249 QPLQIPGGRTVAACDLQGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLHYKRLTTP 308
Db 312 KPLQLK-NITNSARHLEGLLQKRTKRLGAKDDFMEIKSHIFFSLLINWDDLINKKITPP 370
QY 309 FNPVSGPADLKHFDPEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365
Db 371 FNPVSGPSDLRHFDEFTPEEPVPSSIGRSPSILVTASVKEAAEAFLGFSYAPPMDSFL 430

RESULT 8
US-08-712-709-5
; Sequence 5, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-712-709-5

Query Match 70.4%; Score 1379; DB 1; Length 431;
Best Local Similarity 70.8%; Pred. No. 5.7e-126;
Matches 255; Conservative 51; Mismatches 50; Indels 4; Gaps 2;
QY 9 PPSQPSRANGNINLGSANPNARPTDFLKVIGKNGYKVLAKRSDGAFYAVKVLQK 68
Db 73 PPSPPSPSQ-QINLGPSSNPHAKPSDFHLKVLKVGSGFGKVLARHKAEEVFYAVKVLQK 131
QY 69 KSLTKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 128
Db 132 KALKKKEKHMSERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 191
QY 129 RRELEPRARFYTAEVASAIYGLHSLNIIYRDLPENILDCQGHVLTDFGLCKEVEPE 188
Db 192 RCLEPRARSYAEIASALYGLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHN 251
QY 189 ETTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFTNTDVAQMYENILH 248
Db 252 STTSTFCGTPPEYLAPEVLKPEYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 311
QY 249 QPLOIPGGRTVAACDLLOGLLHKDQORLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308
Db 312 KPLQKPNITNSARHLLGLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLLINKKITPP 371
QY 309 FNPVNEGPDALKHFDPEFTQEAHSVKSIGCTPTDV---ASSSGASSAFLGFSYAQDDDDIL 365
Db 372 FNPVSGPNDLRHFDPEFTPEEPVNSIGKSPSVLVTASVKEAAEAFLGFSYAPPTDSDL 431

RESULT 9
US-09-111-444-5
Sequence 5, Application US/09111444
Patent No. 6045792
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-111-444-5

Query Match 70.4%; Score 1379; DB 2; Length 431;
Best Local Similarity 70.8%; Pred. No. 5.7e-126;
Matches 255; Conservative 51; Mismatches 50; Indels 4; Gaps 2;
QY 9 PPSQPSRANGNINLGSANPNARPTDFLKVIGKNGYKVLAKRSDGAFYAVKVLQK 68
Db 73 PPSPPSPSQ-QINLGPSSNPHAKPSDFHLKVLKVGSGFGKVLARHKAEEVFYAVKVLQK 131
QY 69 KSLTKNKEQNHMAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 128
Db 132 KALKKKEKHMSERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 191
QY 129 RRELEPRARFYTAEVASAIYGLHSLNIIYRDLPENILDCQGHVLTDFGLCKEVEPE 188
Db 192 RCLEPRARSYAEIASALYGLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHN 251
QY 189 ETTSTFCGTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMLHGLPPFTNTDVAQMYENILH 248
Db 252 STTSTFCGTPPEYLAPEVLKPEYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 311
QY 249 QPLOIPGGRTVAACDLLOGLLHKDQORLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308
Db 312 KPLQKPNITNSARHLLGLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLLINKKITPP 371
QY 309 FNPVNEGPDALKHFDPEFTQEAHSVKSIGCTPTDV---ASSSGASSAFLGFSYAQDDDDIL 365
Db 372 FNPVSGPNDLRHFDPEFTPEEPVNSIGKSPSVLVTASVKEAAEAFLGFSYAPPTDSDL 431

RESULT 10
US-09-541-228-5
Sequence 5, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: 08/712,709
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
;
US-09-541-228-5

Query Match 70.4%; Score 1379; DB 2; Length 431;
Best Local Similarity 70.8%; Pred. No. 5.7e-126;
Matches 255; Conservative 51; Mismatches 50; Indels 4; Gaps 2;

QY 9 PSPQSRANGNINLGPANPNARPTDFDLKVLKGNKGVLLAKKSPGAFYAVKVLQK 68
DB 73 PSPQSPSQ-QINLGPSSPHAKPSDFHLKVLKIGKSGFGKVLARHAKSEVFYAVKVLQK 131
QY 69 KSLKNKEQHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGELFFHLQRE 128
DB 132 KAILKKKEKHMSERNVLLKNVKHFFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRE 191
QY 129 RFLPEPRARYAEVASAIGYLHSLNIIVRDLPKPNILDCOGHVLTDFGLCKECVEPE 188
DB 192 RCFLEPRARSYAAETASALGYLHSLNIIVRDLPKPNILDSOCHIIVLTFGLCKENIEHN 251
QY 189 ETTSTFCGTPPEYLAPVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFNTDVAQMYENILH 248
DB 252 STTSTFCGTPPEYLAPVLKPEYDRTVDWMCGLGAVLYEMLYGLPPYSRTAEYDNILN 311
QY 249 QPLQIPGGRVTAACDLLOGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLHYHKLTPP 308
DB 312 KPQLKPNITNSARHLEGLLQKRTKRLGAKDDFWEIKSHVFFSLINWDDLINKKITPP 371
QY 309 FNPVNGPADLKHDFEPTQEAIVSKSIGCTPTDV---ASSSGASSAFLGFSYAQDDDDIL 365
DB 372 FNPVNSGPNDLRHFDFEPTPEEPVNSIGKSPSVLVTASVKEAAAEAFLGFSYAPPTDSEL 431

RESULT 11
US-09-771-161A-246
; Sequence 246, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 246
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-771-161A-246
Query Match 44.1%; Score 863; DB 2; Length 479;
Best Local Similarity 48.4%; Pred. No. 1.5e-75;
Matches 171; Conservative 53; Mismatches 107; Indels 22; Gaps 5;

QY 18 GNINLGPSANPNARPT--DFDFLKVIGKGNKGVLLAKKSPGAFYAVKVLQKKSILKNK 75
DB 129 GEEEMDASTTHHKRKTMDNDFYLLKLGKTFGKVLVREKASGKYVAMKILKEVIAKD 188
QY 76 EQNHMAERNVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGELFFHLQRRERLEPR 135
DB 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSERFSEDR 247
QY 136 ARFYTAEVASAIGYLHSLNIIVRDLPKPNILDCOGHVLTDFGLCKECVEPEETTSTFC 195
DB 248 TRFYGAIVSALDYHSGKIVYRDLPKPNILDCOGHVLTDFGLCKEGITDAATNKTFC 307
QY 196 GTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFNTDVAQMYENILHQLQIPG 255
DB 308 GTPEYLAPEVLDEDNDYGRAVDWMCGLGAVLYEMLHGLPPFNTDVAQMYENILHQLQIPG 367
QY 256 GRTVAACDLLOGLLHKDQRL--GSKEDFLDIKNHMFPSINWDDLHYHKLTPPFPNPV 314
DB 368 TLLSDAKSLLSGLLIKDPNKRLLGGGPDDAKEIMRHSFFSGVNMQVDYDKLVPPPKPQVT 427
QY 315 GPADLKHDFEPTQEAIVSKSIGCTPTDVASSSGASSAFLGFSYAQDDDDILDS 367
DB 428 SETDTRYFDEEPT---AQTTITITPE-----KYDEGDMCDMN 462

RESULT 12
US-09-771-161A-247
; Sequence 247, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-771-161A-247
Query Match 44.1%; Score 863; DB 2; Length 479;
Best Local Similarity 48.4%; Pred. No. 1.5e-75;
Matches 171; Conservative 53; Mismatches 107; Indels 22; Gaps 5;

QY 18 GNINLGPSANPNARPT--DFDFLKVIGKGNKGVLLAKKSPGAFYAVKVLQKKSILKNK 75
DB 129 GEEEMDASTTHHKRKTMDNDFYLLKLGKTFGKVLVREKASGKYVAMKILKEVIAKD 188

QY 76 EQNHMAERNVLLKNVRHPELVGLRYSFOTPEKLYFVLDYVNGGELFFHLQRRERFLEPR 135
Db 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLRSRVFSEDR 247
QY 136 ARFYTAEVAISAIGVLSHNLIIYRDLKPENILLDCQGHVLTDFGLCKECVEPETTSTFC 195
Db 248 TRFYGAIEVSALDYLSHGKIVYRDLKLENMLDKGHIKITDFGLCKEGITDAATWKTF 307
QY 196 GTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPPFFNTDVAQMYENILHQLQIPG 255
Db 308 GTPPEYLAPEVLEDNDYGRAVDMWGLGVVYEMWCGRLPFYNQDHEKLFELILMEDIKFPR 367
QY 256 GRTVAACDLLOGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLYHKRLTPFPNPV 314
Db 368 TLSSDAKSLLSGLLIKDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVT 427
QY 315 GPADLKHDFEPTQEAHSVKSIGCTPDTVASSGASSAFGLGFSYAQDDDDILDS 367
Db 428 SETDTRYFDEEFT---AQITITTPPE-----KYDEBGMDCMDN 462

RESULT 13
US-09-771-161A-248
; Sequence 248, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 248
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-248

Query Match 44.1%; Score 863; DB 2; Length 479;
Best Local Similarity 48.4%; Pred. No. 1.5e-75;
Matches 171; Conservative 53; Mismatches 107; Indels 22; Gaps 5;

QY 18 GNINLGPSANPNARPT--DFDFLKVIKGNKYGVLLAKRKS DGAFYAVKVKQKSLKNK 75
Db 129 GEEEMDASTTHHKRTMNDFDYLLKLGKTFGKVILVREKASGYAMKILKKEVIK 188
QY 76 EQNHMAERNVLLKNVRHPELVGLRYSFOTPEKLYFVLDYVNGGELFFHLQRRERFLEPR 135
Db 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLRSRVFSEDR 247
QY 136 ARFYTAEVAISAIGVLSHNLIIYRDLKPENILLDCQGHVLTDFGLCKECVEPETTSTFC 195
Db 248 TRFYGAIEVSALDYLSHGKIVYRDLKLENMLDKGHIKITDFGLCKEGITDAATWKTF 307
QY 196 GTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPPFFNTDVAQMYENILHQLQIPG 255
Db 308 GTPPEYLAPEVLEDNDYGRAVDMWGLGVVYEMWCGRLPFYNQDHEKLFELILMEDIKFPR 367
QY 256 GRTVAACDLLOGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLYHKRLTPFPNPV 314
Db 368 TLSSDAKSLLSGLLIKDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVT 427
QY 315 GPADLKHDFEPTQEAHSVKSIGCTPDTVASSGASSAFGLGFSYAQDDDDILDS 367
Db 428 SETDTRYFDEEFT---AQITITTPPE-----KYDEBGMDCMDN 462

RESULT 14
US-09-526-043-2
; Sequence 2, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-526-043-2

Query Match 43.9%; Score 860; DB 2; Length 465;
Best Local Similarity 51.6%; Pred. No. 2.8e-75;
Matches 164; Conservative 50; Mismatches 100; Indels 4; Gaps 3;

QY 18 GNINLGPSANPNARPT--DFDFLKVIKGNKYGVLLAKRKS DGAFYAVKVKQKSLKNK 75
Db 129 GEEEMDASTTHHKRTMNDFDYLLKLGKTFGKVILVREKASGYAMKILKKEVIK 188
QY 76 EQNHMAERNVLLKNVRHPELVGLRYSFOTPEKLYFVLDYVNGGELFFHLQRRERFLEPR 135
Db 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLRSRVFSEDR 247
QY 136 ARFYTAEVAISAIGVLSHNLIIYRDLKPENILLDCQGHVLTDFGLCKECVEPETTSTFC 195
Db 248 TRFYGAIEVSALDYLSHGKIVYRDLKLENMLDKGHIKITDFGLCKEGITDAATWKTF 307
QY 196 GTPPEYLAPEVLKPEYDRAVDMWCLGAVLYEMHLGLPPFFNTDVAQMYENILHQLQIPG 255
Db 308 GTPPEYLAPEVLEDNDYGRAVDMWGLGVVYEMWCGRLPFYNQDHEKLFELILMEDIKFPR 367
QY 256 GRTVAACDLLOGLLHKDQORL-GSKEDFLDIKNHMFSPINWDDLYHKRLTPFPNPV 314
Db 368 TLSSDAKSLLSGLLIKDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVT 427
QY 315 GPADLKHDFEPTQEAHSVKSIGCTPDTVASSGASSAFGLGFSYAQDDDDILDS 367
Db 428 SETDTRYFDEEFT---AQITITTPPE-----KYDEBGMDCMDN 462

RESULT 15
US-09-526-043-17
; Sequence 17, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 17
; LENGTH: 454
; TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-526-043-17

Query Match          43.8%; Score 858; DB 2; Length 454;
Best Local Similarity 51.6%; Pred. No. 4.2e-75;
Matches 164; Conservative 50; Mismatches 100; Indels 4; Gaps 3;

Qy 18 GNINLGPSANPNARPT--DFDFLKVIKGNYGKVKLLAKRKSDGAFYAVKVLQKKSLKNK 75
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 76 EQNHMAERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGELFFHLQRRRLEPR 135
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 189 EVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRERFSEDR 247
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 136 ARFYTAEVASAIQYLHSLNIIVRDLPENILLDCQGHVVLTDGFLCKECVPEETTSTFC 195
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 248 TRFYGAIEIVSALDYLHSGKIVYRDLEKLEMLDKOGHIKITDFGLCKEGITDAATWKTC 307
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 196 GTPPYLAPEVLKPEYDRAVDWMCLGAVLYEMLHGLPPFFENTDVAQMYENILHQLPIQG 255
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 308 GTPPYLAPEVLENDYGRAVDWMLGAVVYEMWMCGRLPFYNDHEKLFELILMEDIKFPR 367
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 256 GRTVAACDILLOGLLHKOQRLL-GSKEDFLDIKNHMFSPINWDDLYHKRLTPPFNPVE 314
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 368 TLSSDAKSLLSGLLIIDPNKRLGGPDPKKEINRHSFFSGVNMQDYYDKLVPPPKPQVT 427
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 315 GPADLKHFDPEFTOEAVS 332
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 428 SETDTRYFDEEFTAQIT 445
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Search completed: January 27, 2006, 23:33:30
Job time : 18.3113 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:31:20 ; Search time 64.3981 Seconds
(without alignments)
2381.178 Million cell updates/sec

Title: US-09-868-131A-3
Perfect score: 1959
Sequence: 1 MASSPVGVSPQPSRANGNI.....ASSAFGLFSYAQDDDLDS 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	94.3	367	3	US-09-971-118-2
2	1848	94.3	367	4	US-10-291-172-256
3	1848	94.3	367	4	US-10-429-160-52
4	1848	94.3	367	4	US-10-221-278-256
5	1848	94.3	367	4	US-10-380-235-6
6	1848	94.3	382	4	US-10-296-115-1109
7	1848	94.3	396	5	US-10-526-543-83
8	1848	94.3	427	5	US-10-753-267-126
9	1674.5	85.5	398	4	US-10-262-511-140
10	1387	70.8	388	4	US-10-131-410-104
11	1387	70.8	407	4	US-10-067-977-4
12	1387	70.8	407	4	US-10-827-272-4
13	1387	70.8	431	3	US-09-981-353-7
14	1387	70.8	431	4	US-10-403-161-2
15	1387	70.8	431	4	US-10-403-161-4
16	1387	70.8	445	4	US-10-067-977-2
17	1387	70.8	445	4	US-10-827-272-2
18	1387	70.8	526	4	US-10-094-749-1861
19	1383	70.6	431	4	US-10-000-039-2
20	1383	70.6	431	4	US-10-353-690-12
21	1383	70.6	431	5	US-10-756-149-5279
22	1383	70.6	431	6	US-11-044-570-2
23	1381.5	70.5	594	5	US-10-732-923-10768
24	1380.5	70.5	430	3	US-09-810-808-9
25	1379	70.4	431	3	US-09-810-808-5
26	1377.5	70.3	433	5	US-10-732-923-10767
27	1325.5	67.7	340	4	US-10-217-555-17

28	1325.5	67.7	340	4	US-10-217-555-17	Sequence 17, Appl
29	1297.5	66.2	429	4	US-10-295-027-116	Sequence 116, App
30	1297.5	66.2	496	3	US-09-784-249-2	Sequence 2, Appli
31	1297.5	66.2	496	3	US-09-764-875-746	Sequence 746, App
32	1297.5	66.2	496	3	US-09-764-875-900	Sequence 900, Appl
33	1297.5	66.2	496	5	US-10-737-450-4	Sequence 4, Appli
34	1286.5	65.7	496	4	US-10-755-889-42	Sequence 42, Appl
35	1141.5	58.3	308	4	US-10-664-421-85	Sequence 85, Appl
36	1141.5	58.3	308	5	US-10-941-635-85	Sequence 85, Appl
37	981	50.1	422	4	US-10-369-493-7027	Sequence 7027, Ap
38	863	44.1	479	3	US-09-771-161A-246	Sequence 246, App
39	863	44.1	479	3	US-09-771-161A-247	Sequence 247, App
40	863	44.1	479	3	US-09-771-161A-248	Sequence 248, App
41	863	44.1	479	4	US-10-394-322A-3	Sequence 3, Appli
42	863	44.1	479	4	US-10-217-574-33	Sequence 33, Appl
43	863	44.1	479	4	US-10-217-555-33	Sequence 33, Appl
44	863	44.1	479	5	US-10-753-267-108	Sequence 108, App
45	860	43.9	465	3	US-09-526-043-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-971-118-2
; Sequence 2, Application US/09971118
; Patent No. US20020123056A1
; GENERAL INFORMATION:
; APPLICANT: DELANEY, ALLEN
; APPLICANT: YOGANATHAN, THILLAINATHAN
; TITLE OF INVENTION: SGR2 AND ITS USES
; FILE REFERENCE: KINE025CIP
; CURRENT APPLICATION NUMBER: US/09/971,118
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/21479
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-118-2

Query Match	94.3%;	Score	1848;	DB	3;	Length	367;
Best Local Similarity	94.3%;	Pred. No.	4.8e-140;				
Matches	345;	Conservative	10;	Mismatches	11;	Indels	0;
		Gaps	0;				
QY	1	MASSPVGVSPQPSRANGNINILGPSANPNARPTDPLKVIKGNKGVLLAKRKSDDGAF	60				
Db	1	MNSSFAGTSPQPSRANGNINILGPSANPNARPTDPLKVIKGNKGVLLAKRKSDDGAF	60				
QY	61	YAVKVLQKKSILKNEQNHMAERNVLLKNVRHPLVGLRYSFQTEPKLYFVLDYVNGGE	120				
Db	61	YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPLVGLRYSFQTEPKLYFVLDYVNGGE	120				
QY	121	LFPHLQRRRFLPRARFYTAASVAGYLSHLSNIIYRLKPNILLDCQGHVLTDFGL	180				
Db	121	LFPHLQRRRFLPRARFYTAASVAGYLSHLSNIIYRLKPNILLDCQGHVLTDFGL	180				
QY	181	CKECVEPETTSTFCGTPPEYLAPEVLKPEPYDRAVDWVCIGAVLYEMLHGLPPFFNTDVA	240				
Db	181	CKECVEPETTSTFCGTPPEYLAPEVLKPEPYDRAVDWVCIGAVLYEMLHGLPPFFNTDVA	240				
QY	241	QMYENILHLOPLPGGRTVAACDLQLGLHKDQORLGSKEBDFLDIKNHFFSPINWDDL	300				
Db	241	QMYENILHLOPLPGGRTVAACDLQLGLHKDQORLGSKEBDFLDIKNHFFSPINWDDL	300				
QY	301	YHKRLTTPPNPNVEGADLKHPDPTQBAVSKSGICTPDTVAASSGASSAFGLGFSYAQD	360				
Db	301	YHKRLTTPPNPNVTGPADLKHPDPTQBAVSKSGICTPDTVAASSGASSAFGLGFSYAPE	360				

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QY 361 DDILD 366
DB 361 DDILD 366

RESULT 2
US-10-291-172-256
; Sequence 256, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 256
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-256

Query Match 94.3%; Score 1848; DB 4; Length 367;
Best Local Similarity 94.3%; Pred. No. 4.8e-140;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVPSPPSRANGINLGPANPNARPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
DB 1 MNSSPAGTSPQPSRANGINLGPANPNARPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
DB 61 YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180
QY 181 CKECVEPEETSTFCGTPPEYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
DB 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
QY 241 QMYENILHQPLOIPGGRTVAAACDLQLGLHKDQORQLGSKEDFLDIKNHMFSPINWDDL 300
DB 241 QMYENILHQPLOIPGGRTVAAACDLQLGLHKDQORQLGSKEDFLDIKNHMFSPINWDDL 300
QY 301 YHKRLTPPNPNVEGPADLKHPDPEFTQEA VSKSIGCTPDTTVASSSGASSAFLGFSYAQD 360
DB 301 YHKRLTPPNPNVTGPADLKHPDPEFTQEA VSKSIGCTPDTTVASSSGASSAFLGFSYAPE 360
QY 361 DDILD 366
DB 361 DDILD 366

RESULT 3
US-10-429-160-52
; Sequence 52, Application US/10429160
; Publication No. US20040023276A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Teresa R
; APPLICANT: Mao, Mao
; APPLICANT: Linsley, Peter S
; APPLICANT: Lund, Lund
; TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
; FILE REFERENCE: RS0200
; CURRENT APPLICATION NUMBER: US/10/429,160
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/377,714
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-160-52

Query Match 94.3%; Score 1848; DB 4; Length 367;
Best Local Similarity 94.3%; Pred. No. 4.8e-140;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVPSPPSRANGINLGPANPNARPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
DB 1 MNSSPAGTSPQPSRANGINLGPANPNARPTDFDLKVIKGNVGVKLLAKRKS DGAF 60
QY 61 YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
DB 61 YAVKVLQKKSILKKEQSHMAERSVLLKNVRHPPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180
QY 181 CKECVEPEETSTFCGTPPEYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
DB 181 CKEGVEPEDTSTFCGTPPEYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFNTDVA 240
QY 241 QMYENILHQPLOIPGGRTVAAACDLQLGLHKDQORQLGSKEDFLDIKNHMFSPINWDDL 300
DB 241 QMYENILHQPLOIPGGRTVAAACDLQLGLHKDQORQLGSKEDFLDIKNHMFSPINWDDL 300
QY 301 YHKRLTPPNPNVEGPADLKHPDPEFTQEA VSKSIGCTPDTTVASSSGASSAFLGFSYAQD 360
DB 301 YHKRLTPPNPNVTGPADLKHPDPEFTQEA VSKSIGCTPDTTVASSSGASSAFLGFSYAPE 360
QY 361 DDILD 366
DB 361 DDILD 366
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[illegible]

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RESULT 7
US-10-926-543-83
; Sequence 83, Application US/10926543
; Publication No. US20050048589A1
; GENERAL INFORMATION:
; APPLICANT: Jendoubi, Moncef
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCE, THEIR
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND DISEASE
; TITLE OF INVENTION: MANAGEMENT OF LUNG CANCER
; FILE REFERENCE: 705403.4004
; CURRENT APPLICATION NUMBER: US/10/926.543
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US 60/497,790
; PRIOR FILING DATE: 2003-08-25
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-543-83

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Query Match	94.3%	Score 1848;	DB 5;	Length 396;
Best Local Similarity	94.3%;	Pred. No. 5.3e-140;		
Matches 345;	Conservative 10;	Mismatches 11;	Indels 0;	Gaps 0;

Qy	1	MASSPVGVSPSPS	RANGNINLGPSANP	APTFDFELKVI	GKNGYKVLAKR	KSDGAF	60
Db	30	MNSPPAGTSPSPS	RANGNINLGPSANP	NAQTDFDFELKVI	GKNGYKVLAKR	KSDGAF	89
Qy	61	YAVKVLQKKSII	LKNKEQNHI	MAERNVLLKNVR	HPLVGLRYS	FQTPPEKLYFVLDY	NGGSE 120
Db	90	YAVKVLQKKSII	LKKKEQSHI	MAERSVLLKNVR	HPLVGLRYS	FQTPPEKLYFVLDY	NGGSE 149
Qy	121	LPFHLQRRRR	FLPRARFYTA	EVASAI	GLYHSLNIIYRDL	IKPENILDDCGHVV	LDTFGL 180

RESULT 8
US-10-753-267-126
; Sequence 126, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:

QY 301 YHKLTPPPNPNVEGPADLKHDFEFTQEAQVSKSIGCTPDTVASSSGASSAFIAGFSYAQD 360
Db 361 YHKLTPPPNPNVTGPADLKHDFEFTQEAQVSKSIGCTPDTVASSSGASSAFIAGFSYAPE 420
QY 361 DDILD 366
Db 421 DDILD 426

RESULT 9

US-10-262-511-140
; Sequence 140, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomik R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSequidist version 0.1
; SEQ ID NO 140
; LENGTH: 398
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-262-511-140
Query Match 85.5%; Score 1674.5; DB 4; Length 398;
Best Local Similarity 86.9%; Pred. No. 4.6e-126; Indels 29; Gaps 1;
Matches 318; Conservative 9; Mismatches 10;
QY 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKSDGAF 60
Db 61 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKSDGAF 120
QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 120
Db 121 YAVKVLQKKSILKKKEQSHMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE 180
QY 121 LPFHLOERRERLEPRARFYTAEVASAIYGLHSNIIYRDLKPENILLDCQGHVLTDFGL 180
Db 181 LPFHLOERRERLEPRARFYAAEVASAIYGLHSNIIYRDLKPENILLDCQ----- 230
QY 181 CKECVEPEETTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCILGAVLYEMLHGLPFFNTDVA 240
Db 231 -----YLAPEVLKPEPYDRAVDWMCILGAVLYEMLHGLPFFYSQDVS 271
QY 241 QMYENILHQPLOIPGORTVAACDLLOGLLHKQORQLGSKEDFLDKNHFPPSPINWDDL 300
Db 272 QMYENILHQPLOIPGORTVAACDLLOGLLHKQORQLGSKADFLKIKNHFVFFSPINWDDL 331
QY 301 YHKRLTPPNPNVEGPADLKHDFEFTQEAQVSKSIGCTPDTVASSSGASSAFIAGFSYAQD 360
Db 332 YHKRLTPPNPNVTGPADLKHDFEFTQEAQVSKSIGCTPDTVASSSGASSAFIAGFSYAPE 391
QY 361 DDILD 366
Db 392 DDILD 397
RESULT 10
US-10-131-410-104
; Sequence 104, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-104
Query Match 70.8%; Score 1387; DB 4; Length 388;
Best Local Similarity 71.1%; Pred. No. 5.4e-103;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;
QY 9 BSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNKGKVLAKRKSDGAFYAVKVLQK 68
Db 30 PSPPPSPSQ-QINLGPSNPHAKPSDFHLKVIKGNKGKVLAKRKSDGAFYAVKVLQK 88
QY 69 KSLKNKEQHMAERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGELFFHLORE 128

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Db      89 KAILKKKEKHMSERNVLLKNVHFLVGLHFSFQTADKLYFVLDYINGGELFHYLQRE 148
      129 RRFLEPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVVLTDFGLCKECVEPE 188
      149 RCFLEPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDFGLCKENIEHN 208
      189 ETTSTFCGTPHYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPPFNTDVAQMYENILH 248
      209 STTSTFCGTPHYLAPEVLHQPYDRVDWCLGAVLYEMLYGLPPFSRNTAEYDNILN 268
      249 QLOIPIGGRTVAACDLLOGLLHKDQRIQSGKEDFLDIKNHMFESPINWDDLYHKRLTTP 308
      269 KPLQLKPNITNSARHLLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLIINKKITPP 328
      309 FNPVNEGPGADLKHDFPEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDTL 365
      329 FNPVNSGPNDLRHDFPEFTPEEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSDL 388

RESULT 11
US-10-067-977-4
; Sequence 4, Application US/10067977
; Publication No. US20030157679A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-4
Query Match      70.8%; Score 1387; DB 4; Length 407;
Best Local Similarity 71.1%; Pred. No. 5.8e-103;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;
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QY      9 PSPQPSRANGNINLGSANPNARPTDFDLKVIKGNYGKVLAKRSGDGFAYAVKVLQK 68
Db      49 PSPPPSPSQ-QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 107
QY      69 KSILKNKEQNHIAMERNVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYVNGGELFHYLQRE 128
Db      108 KAILKKKEKHMSERNVLLKNVHPPFLVGLHFSFQTADKLYFVLDYINGGELFHYLQRE 167
QY      129 RRFLEPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVVLTDFGLCKECVEPE 188
Db      168 RCFLEPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDFGLCKENIEHN 227
QY      189 ETTSTFCGTPHYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPPFNTDVAQMYENILH 248
Db      228 STTSTFCGTPHYLAPEVLHQPYDRVDWCLGAVLYEMLYGLPPFSRNTAEYDNILN 287
QY      249 QLOIPIGGRTVAACDLLOGLLHKDQRIQSGKEDFLDIKNHMFESPINWDDLYHKRLTTP 308
Db      288 KPLQLKPNITNSARHLLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLIINKKITPP 347
QY      309 FNPVNEGPGADLKHDFPEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDTL 365
Db      348 FNPVNSGPNDLRHDFPEFTPEEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSDL 407

RESULT 12
US-10-827-272-4
; Sequence 4, Application US/10827272
; Publication No. US20040203127A1
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; GENERAL INFORMATION:
; APPLICANT: KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001313-DIV
; CURRENT APPLICATION NUMBER: US/10/827,272
; CURRENT FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-827-272-4
Query Match      70.8%; Score 1387; DB 4; Length 407;
Best Local Similarity 71.1%; Pred. No. 5.8e-103;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;

QY      9 PSPQPSRANGNINLGSANPNARPTDFDLKVIKGNYGKVLAKRSGDGFAYAVKVLQK 68
Db      49 PSPPPSPSQ-QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 107
QY      69 KSILKNKEQNHIAMERNVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYVNGGELFHYLQRE 128
Db      108 KAILKKKEKHMSERNVLLKNVHPPFLVGLHFSFQTADKLYFVLDYINGGELFHYLQRE 167
QY      129 RRFLEPRARFYTAEVASAIQYLHSLNIIYRDLKPNILLDCQGHVVLTDFGLCKECVEPE 188
Db      168 RCFLEPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDFGLCKENIEHN 227
QY      189 ETTSTFCGTPHYLAPEVLKPEYDRADVWCLGAVLYEMLHGLPPFNTDVAQMYENILH 248
Db      228 STTSTFCGTPHYLAPEVLHQPYDRVDWCLGAVLYEMLYGLPPFSRNTAEYDNILN 287
QY      249 QLOIPIGGRTVAACDLLOGLLHKDQRIQSGKEDFLDIKNHMFESPINWDDLYHKRLTTP 308
Db      288 KPLQLKPNITNSARHLLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLIINKKITPP 347
QY      309 FNPVNEGPGADLKHDFPEFTQEAIVSKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDTL 365
Db      348 FNPVNSGPNDLRHDFPEFTPEEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSDL 407

RESULT 13
US-09-981-353-7
; Sequence 7, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1
US-09-981-353-7
Query Match      70.8%; Score 1387; DB 3; Length 431;
Best Local Similarity 71.1%; Pred. No. 6.1e-103;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;

QY      9 PSPQPSRANGNINLGSANPNARPTDFDLKVIKGNYGKVLAKRSGDGFAYAVKVLQK 68
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Db 73 PPSPPSPSQ-QINLGPSNPHAKSPDFHFLKVIKGSFGKVLARHKAEEVFAVAVKLOK 131
Qy 69 KSILKKEONHMAERNVLLKNVRHPFLVGLRYSFQTPKLYFVLDVYNGGELFFHLORE 128
Db 132 KAILKKEKHIMSERVLLKNVHPFLVGLHFSFQTADKLYFVLDVYNGGELFFHLORE 191
Qy 129 RRFLEPRARFYTAESAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECVEPE 188
Db 192 RCFLEPRARFYAAEIASALGTLHSLNIVYRDLKPENILLDSQGHIVLTDFGLCKENIEHN 251
Qy 189 ETTSTFCGTPEYLAPEVLRKEPYDRAVDWNCGLGAVLYEMHLGLPPFFNTDVAQMYENILH 248
Db 252 STTSTFCGTPEYLAPEVLRKEPYDRTVDWNCGLGAVLYEMLYGLPPFYSRNTAEYDNLN 311
Qy 249 QPLQIPGGRRTVAACDLLOGLLHKDQOROLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308
Db 312 KPLQLKKNITNSARHLLEGLLQKDRTRLGAKODFMEIKSHVFFSLINWDDLINKKITPP 371
Qy 309 FNPVVEGPADLKHDFPFTQEAHSVKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365
Db 372 FNPVSGNDLRHDFPFTQEAHSVKSIGSPDSVLTASVKEAAEAFLGFSYAPPTDSFL 431

RESULT 14

US-10-403-161-2
; Sequence 2, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403.161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2

LENGTH: 431
TYPE: PRT

ORGANISM: Homo sapiens

US-10-403-161-2

Query Match 70.8%; Score 1387; DB 4; Length 431;
Best Local Similarity 71.1%; Pred. No. 6.1e-103;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;
Qy 9 PPSPPSRANGINLGPSANPNARPTDFDLKVIKGSFGKVLARHKAEEVFAVAVKLOK 68
Db 73 PPSPPSPSQ-QINLGPSNPHAKSPDFHFLKVIKGSFGKVLARHKAEEVFAVAVKLOK 131
Qy 69 KSILKKEONHMAERNVLLKNVRHPFLVGLRYSFQTPKLYFVLDVYNGGELFFHLORE 128
Db 132 KAILKKEKHIMSERVLLKNVHPFLVGLHFSFQTADKLYFVLDVYNGGELFFHLORE 191
Qy 129 RRFLEPRARFYTAESAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECVEPE 188
Db 192 RCFLEPRARFYAAEIASALGTLHSLNIVYRDLKPENILLDSQGHIVLTDFGLCKENIEHN 251

Qy 129 RRFLEPRARFYTAESAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECVEPE 188
Db 192 RCFLEPRARFYAAEIASALGTLHSLNIVYRDLKPENILLDSQGHIVLTDFGLCKENIEHN 251
Qy 189 ETTSTFCGTPEYLAPEVLRKEPYDRAVDWNCGLGAVLYEMHLGLPPFFNTDVAQMYENILH 248
Db 252 STTSTFCGTPEYLAPEVLRKEPYDRTVDWNCGLGAVLYEMLYGLPPFYSRNTAEYDNLN 311
Qy 249 QPLQIPGGRRTVAACDLLOGLLHKDQOROLGSKEDFLDIKNHMFSPINWDDLYHKRLTTP 308
Db 312 KPLQLKKNITNSARHLLEGLLQKDRTRLGAKODFMEIKSHVFFSLINWDDLINKKITPP 371
Qy 309 FNPVVEGPADLKHDFPFTQEAHSVKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365
Db 372 FNPVSGNDLRHDFPFTQEAHSVKSIGSPDSVLTASVKEAAEAFLGFSYAPPTDSFL 431

RESULT 15

US-10-403-161-4
; Sequence 4, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403.161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4

LENGTH: 431
TYPE: PRT

ORGANISM: Homo sapiens

US-10-403-161-4

Query Match 70.8%; Score 1387; DB 4; Length 431;
Best Local Similarity 71.1%; Pred. No. 6.1e-103;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;
Qy 9 PPSPPSRANGINLGPSANPNARPTDFDLKVIKGSFGKVLARHKAEEVFAVAVKLOK 68
Db 73 PPSPPSPSQ-QINLGPSNPHAKSPDFHFLKVIKGSFGKVLARHKAEEVFAVAVKLOK 131
Qy 69 KSILKKEONHMAERNVLLKNVRHPFLVGLRYSFQTPKLYFVLDVYNGGELFFHLORE 128
Db 132 KAILKKEKHIMSERVLLKNVHPFLVGLHFSFQTADKLYFVLDVYNGGELFFHLORE 191
Qy 129 RRFLEPRARFYTAESAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKECVEPE 188
Db 192 RCFLEPRARFYAAEIASALGTLHSLNIVYRDLKPENILLDSQGHIVLTDFGLCKENIEHN 251

QY	189	ETTSTFCGTPEYL	PEVLRKEPYDRAVDMWCLGAVLYEMHGLPPRENTDVAOMYENILH	248
Db	252	STTSTFCGTPEYL	PEVLRKEPYDRAVDMWCLGAVLYEMHGLPPRENTDVAOMYENILH	311
QY	249	QPLQIPGGR	TVAAACDLIQGLLHKDQRLGSKEDFLDIKNHMFSPINWDDLYHKRLTPP	308
Db	312	KPLQKPNITNS	ARHLLLEGULLQKDRTKRLGAKDDFWEIKSHVFFSLINWDDLINKKITPP	371
QY	309	FNPV	EGPADLKHFDPEFTQEA VSKIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL	365
Db	372	FNPVSGPN	DLRHFDPEFTTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL	431

Search completed: January 27, 2006, 23:57:31
Job time : 64.3981 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:32:16 ; Search time 9.46352 Seconds
(without alignments)
419.957 Million cell updates/sec

Title: US-09-868-131A-3

Perfect score: 1959

Sequence: 1 MASSPVGVPSQPSPRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New*

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1387	70.8	543	6	US-10-821-234-1158
2	847.5	43.3	480	7	US-11-109-156-18
3	794.5	40.6	495	6	US-10-770-726-81
4	750	38.3	737	7	US-11-152-366-28
5	713	36.4	740	6	US-10-878-556A-129
6	705.5	36.0	341	7	US-11-092-168-4
7	698.5	35.7	343	7	US-11-092-168-3
8	697	35.6	351	7	US-11-132-142-13
9	696.5	35.6	462	7	US-11-132-142-10
10	695.5	35.5	351	7	US-11-132-142-14
11	688.5	35.1	942	6	US-10-770-726-76
12	685.5	35.0	350	6	US-10-497-767-4
13	683.5	34.9	381	7	US-11-132-142-9
14	675.5	34.5	393	7	US-11-132-142-12
15	673	34.4	353	7	US-11-132-142-11
16	668	34.1	705	6	US-10-995-561-856
17	668	34.1	706	6	US-10-995-561-855
18	668	34.1	706	7	US-11-099-958-1
19	665	33.9	351	7	US-11-099-958-2
20	662	33.8	398	7	US-11-132-142-7
21	658	33.6	515	7	US-11-132-142-8
22	651.5	33.3	548	7	US-11-132-142-5
23	645	32.9	480	7	US-11-132-142-6
24	535.5	27.3	1732	6	US-10-055-877-147
25	521.5	26.6	1663	6	US-10-055-877-148

26	520.5	26.6	1590	6	US-10-055-877-146	Sequence 146, Appl
27	520	26.5	256	6	US-10-877-346-72	Sequence 72, Appl
28	520	26.5	256	7	US-11-113-424-183	Sequence 183, Appl
29	518	26.4	756	7	US-11-113-837-20	Sequence 20, Appl
30	512.5	26.2	1197	6	US-10-055-877-8	Sequence 8, Appl
31	512.5	26.2	1247	6	US-10-055-877-10	Sequence 10, Appl
32	512	26.1	637	7	US-11-113-837-4	Sequence 4, Appl
33	500	25.5	635	7	US-11-113-837-16	Sequence 16, Appl
34	498	25.4	688	7	US-11-113-424-45	Sequence 45, Appl
35	498	25.4	1613	6	US-10-055-877-145	Sequence 145, Appl
36	498	25.4	1637	6	US-10-055-877-144	Sequence 144, Appl
37	494.5	25.2	668	7	US-11-113-424-12	Sequence 12, Appl
38	492	25.1	639	7	US-11-113-837-21	Sequence 21, Appl
39	488.5	24.9	2053	6	US-10-877-346-11	Sequence 11, Appl
40	488.5	24.9	2066	6	US-10-877-346-9	Sequence 9, Appl
41	487	24.9	688	7	US-11-113-424-48	Sequence 48, Appl
42	485	24.8	688	7	US-11-113-424-49	Sequence 49, Appl
43	484	24.7	396	7	US-11-125-295-11	Sequence 11, Appl
44	484	24.7	407	7	US-11-125-295-9	Sequence 9, Appl
45	475	24.2	689	7	US-11-113-424-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-821-234-1158
; Sequence 1158, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1158
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1158

Query Match	70.8%	Score 1387;	DB 6;	Length 543;
Best Local Similarity	71.1%	Pred. No. 1.6e-120;		
Matches	256;	Conservative	51;	Mismatches 49;
		Indels	4;	Gaps 2;
QY	9	PSPQSRANGNINLGSANPNARPTDFLKVIGKNGYKVLAKRSGDAFYAVKVLQK 68		
Db	185	PSPPSPSQ-QINLGPSSPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 243		
QY	69	KSLTKNKEQNHMAEENVLKNVRHPLCLRSFQTPKLYFVLDYVNGELFFHLORE 128		
Db	244	KALKKBEKHMSERNVLLKNVHPFLGLHFSQTADKLYFVLDYINGELFFHLORE 303		
QY	129	RRPLEPRARFYAEVASAIGYLHSLNIIYRDLPENILLDCQGHVLTDFGLCKECVEPE 188		
Db	304	RCFLEPRARFYAEIASALGYLHSLNIVYRDLPENILLDSQGHVLTDFGLCKENIEHN 363		
QY	189	ETTSTFCGTPEYLAPVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFPNTDVAQMYENILH 248		
Db	364	STTSTFCGTPEYLAPVLRKHQPYDRTVDWVCLGAVLYEMLYGLPPFYSRNTAEMYDNLN 423		
QY	249	QPLQIPGGTVAACDLQGLHKDQORLGSKEDEFLDKNHFESPTNWDLLYHKRLTPP 308		
Db	424	KPLQLKPNITNSARHLLGELQKORTKRGAKDDFMEIKSHVFFSLINWDLLINKKITPP 483		
QY	309	FNPVNBGPADLKHFDPETOEAHSVKSIGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365		


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; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-28

Query Match      38.3%; Score 750; DB 7; Length 737;
Best Local Similarity 41.9%; Pred. No. 1.7e-61;
Matches 157; Conservative 69; Mismatches 115; Indels 34; Gaps 7;

QY 2 ASSPVG-VPSQPSRANGNINLGSANPNARPTDFLKVIGKNGYKVLAKRKSQDAF 60
Db 379 ASSPDGQLMSP---GENGEVRQQAQRLGL--DEFNFIKVLGKSGFGKWLAEILKGDV 433
QY 61 YAVKVLQKSKTLKNKEONHMAERNVLLKNVRHPLVGLRVSFOTPEKLVLDVYNGGE 120
Db 434 YAVKVLKDVILQDDVDCTWTEKRIILALARKHPIYLTQLCCFQTKDRLFFVMEYVNGSD 493
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIYGLHSLNIIYRDLKPNILLDCOQHVVLTDFGL 180
Db 494 LMFQIQRSRKFDEPRSFYAEVTSALMFLHQHGVIRDLKLNILLDAEGHCKLADFGM 553
QY 181 CKECVEPEETSTPCGTPPEYLAPVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFPNTDVA 240
Db 554 CKEGILNGVTTTFCGTPDVIAPBILQLELYGPGSDWWALGVLMYEMWAGQPPPEADNED 613
QY 241 QMVENILHQPLOTIPGGRITVAACDLLOGLLHKDQORLG-----SKDFLDIKNMFPSPI 295
Db 614 DLFESILHDDVLYPVWLVSKEAVSILKAFMTKNPKHRLGCVASONGED--AIKQHPFPKEI 671
QY 296 NWDDLHYHKLTPPPNPNVEGPADLKHFPDPBFTQ-----BAVSKSIGCTPDPVTASS 346
Db 672 DWLLEQKKIKPFPKPIKTRDVNNFDDQFTREBPVLTLDVAIVKQIN----- 721
QY 347 GASSAFGFSYAQDD 361
Db 722 --QBEFKGFSYFGED 734

RESULT 5
US-10-878-556A-129
; Sequence 129, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/k6a3_human
; DATABASE ENTRY DATE: 1996-10-01
US-10-878-556A-129

Query Match      36.4%; Score 713; DB 6; Length 740;
Best Local Similarity 40.3%; Pred. No. 4.6e-58;
Matches 157; Conservative 63; Mismatches 130; Indels 40; Gaps 8;

QY 6 VGVSPQPSRAN-----GNINLCP-----SANPNARPTDFDLK 39
Db 13 MAVESDSSENQQIMDEPWEENINPQTEVSIKEIATHVKEGKADSPSELK 72
QY 40 VIGKNGYKVLAKRKSQD---AFYAVKVLQKSKILKNKEQNHMAERNVLLKNVRHPL 96
Db 73 VLGQSGFGKVLVKKISGSDARQLYAMKVL--KKATLKVDRVTRTKMERDILVE--VNHFFI 130

; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-28

Query Match      38.3%; Score 750; DB 7; Length 737;
Best Local Similarity 41.9%; Pred. No. 1.7e-61;
Matches 157; Conservative 69; Mismatches 115; Indels 34; Gaps 7;

QY 2 ASSPVG-VPSQPSRANGNINLGSANPNARPTDFLKVIGKNGYKVLAKRKSQDAF 60
Db 379 ASSPDGQLMSP---GENGEVRQQAQRLGL--DEFNFIKVLGKSGFGKWLAEILKGDV 433
QY 61 YAVKVLQKSKTLKNKEONHMAERNVLLKNVRHPLVGLRVSFOTPEKLVLDVYNGGE 120
Db 434 YAVKVLKDVILQDDVDCTWTEKRIILALARKHPIYLTQLCCFQTKDRLFFVMEYVNGSD 493
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIYGLHSLNIIYRDLKPNILLDCOQHVVLTDFGL 180
Db 494 LMFQIQRSRKFDEPRSFYAEVTSALMFLHQHGVIRDLKLNILLDAEGHCKLADFGM 553
QY 181 CKECVEPEETSTPCGTPPEYLAPVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFPNTDVA 240
Db 554 CKEGILNGVTTTFCGTPDVIAPBILQLELYGPGSDWWALGVLMYEMWAGQPPPEADNED 613
QY 241 QMVENILHQPLOTIPGGRITVAACDLLOGLLHKDQORLG-----SKDFLDIKNMFPSPI 295
Db 614 DLFESILHDDVLYPVWLVSKEAVSILKAFMTKNPKHRLGCVASONGED--AIKQHPFPKEI 671
QY 296 NWDDLHYHKLTPPPNPNVEGPADLKHFPDPBFTQ-----BAVSKSIGCTPDPVTASS 346
Db 672 DWLLEQKKIKPFPKPIKTRDVNNFDDQFTREBPVLTLDVAIVKQIN----- 721
QY 347 GASSAFGFSYAQDD 361
Db 722 --QBEFKGFSYFGED 734

RESULT 6
US-11-092-168-4
; Sequence 4, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurler, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bears, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-092-168-4

Query Match      36.0%; Score 705.5; DB 7; Length 341;
Best Local Similarity 44.1%; Pred. No. 8e-58;
Matches 138; Conservative 61; Mismatches 107; Indels 7; Gaps 5;

QY 24 PSANPNARPTDFDLKVIKNGYKVLAKRKSQDAFYAVKVLQKSKILKNKEQNHMAE 83
Db 24 PSQN-TAQLDQDFRIKTLGTGSGFGRVLMVKHESGNHYAMKILDKQVVKLQKIEHTLNE 82
QY 84 RNVLKNVRHPLVGLRVSFOTPEKLVYFDVYNGGELFFHLQRRERFLEPRARFYTAEV 143
Db 83 KRI-LQAVNFPFLVKLEFSFKDNLNLYVMVEYVAGGEMFSLRRIGRFAEPHARFYAAQI 141
QY 144 ASAIYGLHSLNIIYRDLKPNILLDCOQHVVLTDFGLCKECVEPEETSTFTFCGTPPEYLAP 203
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Db 142 VLTPEYVHSLDIYRLDKPENLLIDQGGYIQVTDGFAKRV---KGRWTWLTGTPYLA 198
QY 204 EVLRKEPYDRAVDWNCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQLPIPGGRTVAACD 263
Db 199 EILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQYIEKIVSGKVRFPFHFSSDLKD 258
QY 264 LLOGLLHKDQORLGS-KEDFLDIKNHMFSPINWDDLHYKELTPPENPNVGGPADLKH 322
Db 259 LLRNLLQVLDLTKRFGNLKGVNDIKNHWKWFATTDWIAIYQKVEAPFIPKFKGPGDTSNF 318
QY 323 DPEFTQEA VSKSI 335
Db 319 D-DYEEERVS I 330

RESULT 7

US-11-092-168-3
; Sequence 3, Application US/11092168
; Publication No. US2005027658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bears, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; PRIOR FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-092-168-3

Query Match 35.7%; Score 698.5; DB 7; Length 343;
Best Local Similarity 43.5%; Pred. No. 3.6e-57;
Matches 136; Conservative 64; Mismatches 106; Indels 7; Gaps 5;

QY 24 PSANPNARPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQKKSILKNKEQNHIAMAE 83
Db 26 PAQN-TAHLDOFERIKTLTGSGFRVNLVKHKTGNHFMAMKILDKQKVKLKQIEHTINE 84
QY 84 RNVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGELFFHLQRRERFLEPRARFYTAEV 143
Db 85 KRI-LQAVNPPFLVKLEYSKDNLSNLYMVEYVPGEMFSLRRIGRSEPHARFYAAQI 143
QY 144 ASAGVILHSLNIYRDLKPNILLDCQGHVLTDFGLCKECVEPEBTSTTCGTPPYLAP 203
Db 144 VLTPEYVHSLDIYRLDKPENLLIDQGGYIQVTDGFAKRV---KGRWTWLTGTPYLA 200
QY 204 EVLRKEPYDRAVDWNCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQLPIPGGRTVAACD 263
Db 201 EILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQYIEKIVSGKVRFPFHFSSDLKD 260

QY 264 LLOGLLHKDQORLGSKEDFL-DIKNHWFFSPINWDDLHYKELTPPENPNVGGPADLKH 322
Db 261 LLRNLLQVLDLTKRFGNLKGVNDIKNHWKWFATTDWIAIYQKVEAPFIPKFKGPGDTSNF 320
QY 323 DPEFTQEA VSKSI 335
Db 321 D-DYEEERVS I 332
RESULT 8
US-11-132-142-13
; Sequence 13, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-11-132-142-13

Query Match 35.6%; Score 697; DB 7; Length 351;
Best Local Similarity 43.9%; Pred. No. 5e-57;
Matches 133; Conservative 61; Mismatches 103; Indels 6; Gaps 4;

QY 34 DFDFLKVIGKNGYKVLAKRSDGAFYAVKVLQKKSILKNKEQNHIAMERNVLLKNVRH 93
Db 43 DFDRMKTGTGSGFRVNLVKHKGASQYAMKILDKQKVKLKQIEHTLNEKRI-LQAVNF 101
QY 94 PELVGLRYSFOTPEKLYFVLDDYNGGELFFHLQRRERFLEPRARFYTAEVASAGYLHSL 153
Db 102 PELVRLSEYFKDNLSNLYMVEYVPGEMFSLRRIGRSEPHARFYAAQIVLTPEYVHSL 161
QY 154 NIIYRDLKPNILLDCQGHVLTDFGLCKECVEPEBTSTTCGTPPYLAPEVLRKEPYDR 213
Db 162 DLIIYRDLKPNILLDQGGYIQVTDGFAKRV---KGRWTWLTGTPPYLAPEIILSKGYNK 218
QY 214 AVDWNCGLGAVLYEMLHGLPPFFNTDVAQMYENILHQLPIPGGRTVAACDLLOGLLHKDQ 273
Db 219 AVDWALGVLIYEMAAGYPPFFADQPIQYIEKIVSGKVRFPFHFSSDLKDLRNLLQVLD 278
QY 274 RORLGS-KEDFLDIKNHMFSPINWDDLHYKELTPPENPNVGGPADLKHDFDPEFTQEA 332
Db 279 TKRYGNLKNVNDIKNHWKWFATTDWIAIYQKVEAPFIPKFKGPGDTSNF-DYEEEDIR 337
QY 333 KSI 335
Db 338 VSL 340

RESULT 9

US-11-132-142-10
; Sequence 10, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US


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RESULT 12
US-10-497-767-4
; Sequence 4, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOWORKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VP1/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497,767
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (338)
; OTHER INFORMATION: Variable amino acid
US-10-497-767-4
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Query Match 35.0%; Score 685.5; DB 6; Length 350;
Best Local Similarity 42.8%; Pred. No. 5.8e-56;
Matches 134; Conservative 62; Mismatches 110; Indels 7; Gaps 5;
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QY 24 PSANPNARPTDFDLKVGKNGYKVLAKRKS DGAFYAVKVLQKKSILKNKEQNHI MAE 83
DB 33 PAQN-TAHLDDQFERIKTLGTSGSFRVLMVKHMETGNHYAMKILDKQVVKLKQIEHTLNE 91
QY 84 RNVLKNVRHPLFLVGLRYSQTPEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYTAEV 143
DB 92 KRI-LQAVNPFPLVLEKFSFKNSNLVYVNGGEMSHLRIGRFSPEHARFYAAQI 150
QY 144 ASAIGYLHSLNIYRDLKPNILDCQGHVLTDFGLCKECVEPETTTSTFCGTPEYLAP 203
DB 151 VLTFEYLHSLDLIYRDLKPNILLIDQGYIQVTDGFAKRV---KGRTWLTCGTPEYLAP 207
QY 204 EVLRKEPYDRAVDWCLGAVLYEMLHGLPPFFNTDVAQMYENILHQLPQIPGGRVTAACD 263
DB 208 EITLSKGYNKAVDWMALGVLVYEMAAAGYPPFFADQPIQIYEKIVSGKVRFPFSHSDLDK 267
QY 264 LQGLLHKQORQLGS-KEDFLDIKNHMFSPINWDDLYHKRLTTPPNPNVEGPADLKH 322
DB 268 LKRLQLVDLTKRFGNLKGVNDIKNKFATTDITAIYQKVEAPFIPKFGGDTSNF 327
QY 323 DPEFTQEA VSKSI 335
DB 328 D-DYEEIEIRVXI 339
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RESULT 13
US-11-132-142-9
; Sequence 9, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
```

```
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Leishmania sp.
US-11-132-142-9
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Query Match 34.9%; Score 683.5; DB 7; Length 381;
Best Local Similarity 42.0%; Pred. No. 1e-55;
Matches 136; Conservative 65; Mismatches 110; Indels 13; Gaps 5;
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QY 33 TDFDLKVGKNGYKVLAKRKS DGAFYAVKVLQKKSILKNKEQNHI MAERNVLLKNVR 92
DB 70 SDFELKNTLTGSGFRVIAHRKGTETEEYVIAIKLRKEIILKMKQOQHVAKQEKILME-LC 128
QY 93 HPFLVGLRYSQTPEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYTAEVASAIYLHS 152
DB 129 HPFIVNMCSFDDEKVKVFLLEFVNGGEMFTHLRTAGRPNDVAKFYHAELVLAFLYLS 188
QY 153 LNIYRDLKPNILDCQGHVLTDFGLCKECVEPETTTSTFCGTPEYLAPVLRKEPYD 212
DB 189 LDVIYRDLKPNILLDNKGHVMTDFGFAKV---PDRFTLTCGTPEYLAPVIOSKGHG 245
QY 213 RAVDWMLGAVLYEMLHGLPPFFNTDVAQMYENILHQLPQIPGGRVTAACD LLLQGLLHKD 272
DB 246 KAVDWMVGLVLYEYFIAGYPPYDDTPRIYEKILAGRLKFPNWDGRARDLVKGLQTD 305
QY 273 QRQLGS-KEDFLDIKNHMFSPINWDDLYHKRLTTPPNPNVEGPADLKHFDPEFTQEA 331
DB 306 HTKRLGLTKGSPADVKNHPYFHGANWMDKLYARYYPAPVVRVKSPGDTSNFE-KYPDSPV 364
QY 332 SKSIGCTPDTVA SSSGASSAF LGF 355
DB 365 DR-----TPALTSAAQQAELKGF 381
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RESULT 14
US-11-132-142-12
; Sequence 12, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Danio
US-11-132-142-12
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Query Match 34.5%; Score 675.5; DB 7; Length 395;
Best Local Similarity 41.8%; Pred. No. 5.7e-55;
Matches 135; Conservative 58; Mismatches 115; Indels 15; Gaps 5;
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QY 34 DFDLKVIGKNGYKVLAKRKS DGAFYAVKVLQKKSILKNKEQNHI MAERNVLLKNVRH 93
DB 87 DFDKLTLTGSGFRVLMVKHQSQYFAMKILDKLVVKKLQIEHTLNEKKI-LQAVSF 145
QY 94 PFLVGLRYSQTPEKLYFVLDYVNGGELFFHLQRRERFLEPRARFYTAEVASAIYLHSL 153
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Job time : 10.4635 secs

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Db 146 PFLVLECAFKDNLNVMRYIQGGEMFSLRRIGRFSQNRFYAAQIVLTPEYLHML 205
Qy 154 NIIVRDLKPENILLDCQGHVVLTDPLGCKECVEPEETSTFCGTPEYLAPEVLKPEYDR 213
Db 206 DLIYRDLKPENILLIDHGYIQVTDGFAKRV---KGRWTLCGTPEYLAPEIILSKGYNK 262
Qy 214 AVDWMLGVLVYEMHLGHPFFNTDVAQMYENILHQLPIPGGRTVAACDLLOGLLHKDQ 273
Db 263 AVDWMLGVLVYEMHLGHPFFNTDVAQMYENILHQLPIPGGRTVAACDLLOGLLHKDQ 322
Qy 274 RORLGS-KEFDLIDKNHMFSPINWDDLHYKRLTPPNVVEGADLKHFDPEFTQEAUS 332
Db 323 TKRFGNLKNGVSDIKNHRWFASDWMIAIYEKKVDAPIIKRCRGGDTSNFD-EYDEEVR 381
Qy 333 KSIGCTPTVASSSGASSAFLGF 355
Db 382 VSV-----SEQCKEFLDF 395

RESULT 15
US-11-132-142-11
; Sequence 11, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; CURRENT APPLICATION NUMBER: US/11/132,142
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Anopheles sp.
US-11-132-142-11
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Query Match 34.4%; Score 673; DB 7; Length 353;
Best Local Similarity 41.4%; Pred. No. 8 4e-55;
Matches 132; Conservative 67; Mismatches 110; Indels 10; Gaps 6;

Qy 27 NP--NARPTDFDLKVGKNGYKVLAKKSDGAFYAVKVLQKSKILKNKEQHMAER 84
Db 36 NPTNTAALDDFERIKTLGTSGFRVMIVQHKSTKYVAMKILDKQKVKLKQVEHTLNEK 95
Qy 85 NVLLKNVRHPPFLGLRYSPQTPEKLYFVLVDYNGGELFHLQRRERLEPRARPYTAEVA 144
Db 96 RI--LQAISFPFLVSLKFKDNLNVMRYIYVLEYPGGMFSLRRIGRFSQNRFYAAQIV 154
Qy 145 SAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDPLGCKECVEPEETSTFCGTPEYLAPE 204
Db 155 LAPEYLHYLDLIYRDLKPENILLDSQGLYKVTDFGAKRV---KGRWTLCGTPEYLAPE 211
Qy 205 VLKSPYDRAVDWMLGVLVYEMHLGHPFFNTDVAQMYENILHQLPIPGGRTVAACDL 264
Db 212 IILSKGYNKAVDWMALGVLVYEMAGVPPFPADQPIQIYEKIVSGKVRFPSPHSGSELKDL 271
Qy 265 LQGLLHKDQORLGS-KEFDLIDKNHMFSPINWDDLHYKRLTPPNVVEGADLKHFD 323
Db 272 LRNLLQVLDLTKRYGNLKAGVNDIKGHRWFASDWMIAIYEKKVDAPIIKRCRGGDTSNFD 331
Qy 324 PEFTQEA--VSKSIGCTPD 340
Db 332 -DYEETLRISSTKCAKE 349
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Search completed: January 27, 2006, 23:58:24

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:12:00 ; Search time 10.8484 Seconds
(without alignments)
3254.993 Million cell updates/sec

Title: US-09-868-131A-3
Perfect score: 1959
Sequence: 1 MASSPVGVSPQPSRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1389	70.9	431	2 A48094	serum and glucocor
2	981	50.1	422	2 T26334	hypothetical prote
3	863	44.1	479	1 A59380	protein kinase (EC
4	860	43.9	462	1 T17287	protein kinase (EC
5	858	43.8	454	1 JC4345	protein kinase (EC
6	851.5	43.5	480	1 S33364	protein kinase (EC
7	851.5	43.5	763	1 A40831	gag-akt polyprotei
8	851	43.4	481	1 A46288	protein kinase (EC
9	848.5	43.3	480	1 JC2437	protein kinase (EC
10	848	43.3	680	2 S37955	protein kinase YPK
11	847.5	43.3	480	1 A39360	protein kinase (EC
12	845.5	43.2	480	1 S62117	protein kinase (EC
13	837	42.7	481	1 JC2438	protein kinase (EC
14	834	42.6	479	2 A38578	protein kinase 2 (
15	833	42.5	677	2 JS0178	protein kinase YKR
16	827.5	42.2	611	1 A55888	protein kinase (EC
17	795	40.6	481	2 JE0377	p70 S6 kinase (EC
18	794	40.5	569	2 T50414	probable prolifera
19	783.5	40.0	1016	1 A46079	protein kinase C (
20	780.5	39.8	525	1 A41887	ribosomal protein
21	780.5	39.8	525	1 S12906	probable ribosomal
22	778.5	39.7	586	2 A53758	protein kinase C (
23	778.5	39.7	587	2 A49509	protein kinase C (
24	777.5	39.7	546	1 T43233	protein kinase (EC
25	773	39.5	541	1 T43232	protein kinase (EC
26	772.5	39.4	646	2 T38171	probable serine/th
27	771.5	39.4	525	1 TVR276	ribosomal protein
28	768	39.2	634	1 B32392	protein kinase C (
29	763	38.9	592	2 JN0877	protein kinase C (

ALIGNMENTS

RESULT 1

A48094
serum and glucocorticoid-regulated kinase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A48094
R;Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.
Mol. Cell. Biol. 13, 2031-2040, 1993
A;Title: Characterization of sgk, a novel member of the serine/threonine protein kinase
A;Reference number: A48094; MUID:93204949; PMID:8455596
A;Accession: A48094
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-431 <WEB>
A;Cross-references: UNIPARC:UPR000017A3E8
A;Experimental source: Con5.hdc mammary epithelial tumor cells
A;Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBIPI:127619)
C;Keywords: ATP
F;96-355/Domain: protein kinase homology <KIN>
F;104-112/Region: protein kinase ATP-binding motif

Query Match	70.9%;	Score	1389;	DB 2;	Length	431;			
Best Local Similarity	71.1%;	Pred. No.	2.3e-58;						
Matches	256;	Conservative	53;	Mismatches	47;	Indels	4;	Gaps	2;
QY	9	PSQPQRANGNINLPSANPNARPTDFDLKVIKGNVKGVLAKRSDGAFYAVKVLQK	68						
Db	73	PSPPSPSQ-QINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEAFYAVKVLQK	131						
QY	69	KSILKNKEQHINMAERNVLLKNVRHDFLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE	128						
Db	132	KAILKKKEKHIMSEKRVLLKNVHFPFLVGLHFSQTDKLYFVLDYINGGELFYHLORE	191						
QY	129	RFLPRARFYAEVASAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGLCKECVEPE	188						
Db	192	RCFLEPRARFYAEIASALGYLHSLNIVYRDLKPNILLDSQQGHI VLTDFGLCKENIEHN	251						
QY	189	ETTSTFCGTPYLAPEVLKRPYDRAVDWVCGLAVLYEMLHGLPFPFNTDVAQMYENILH	248						
Db	252	GTTSTFCGTPYLAPEVLKRPYDRTVDWVCGLAVLYEMLYGLPFPVSRNTAEYDNLN	311						
QY	249	QPLQIPGGTVAACDLGLLHKDQORLGSKEDFLDKNMHFFSINWDDLHYKRLTTPP	308						
Db	312	KPLQLKPNITNSARHLEGLLQKORTKRLGAKDDFMEIKSHIFPSLINWDDLINKKITPP	371						
QY	309	FNPVNEGADLKHFDPEFTQEAHSVKSIGCTPPTV---ASSSGASSAPLGFSAQDDDDIL	365						
Db	372	FNPVSGPSDLRHRDFEFTTEBPVSSIGRSPSILVTASVKEAEEAFLGFSAAPPMDSFL	431						
RESULT 2									
T26334									

RESULT 2

T26334

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F;4-105/Domain: pleckstrin repeat homology <PLK>
F;146-405/Domain: protein kinase homology <KIN>
F;154-162/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted

Query Match 43.9%; Score 860; DB 1; Length 462;
Best Local Similarity 51.6%; Pred. No. 1.1e-33;
Matches 164; Conservative 50; Mismatches 100; Indels 4; Gaps 3;

QY 18 GNINLGPSANPNARPT--DFDFLVKVGKNGYKVLAKRKSDGAFYAVKVLQKKSILKNK 75

DB 129 GEEEMDASTTHKKRTKNDPDLKLGKTFGKVLVREKASGYAMKILKEVIAKD 188

QY 76 EQNHMAERNVLLKNVRHPLVGLRYSFQPEKLYFVLDYVNGGELFFHLQRRRRFLEPR 135

DB 189 EVAHTLTESRV-LKNTRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLRSRVFSEDR 247

QY 136 ARFYTAEVASAGLYHSLNIIYRDLPENILLDCQGHVLTDFGLCKECVEPEETTTSTFC 195

DB 248 TRFYGABIVSALDYLHSGKIVYRDLEKLENMLDKDGHKITDFGLCKEGITDAATMTKTC 307

QY 196 GTPPYLAPEVLKPEPYDRAVDWMLGAVLYEMHLGLPFFNTDVAQMYENILHQPQLQIPG 255

DB 308 GTPPYLAPEVLEDNDYGRAVDWMLGAVLYEMHCGRLPFFYNQDHEKLFELIMEDIKPPR 367

QY 256 GRTVAACDLLOGLLHKDQORL-GSKEDFLDKNHHMFSPINWDDLHYKRLTPPFPNVE 314

DB 368 TLSSDAKSLSLGLLIKDPNKRLLGGPDPAKEIMRHSFFSGVNWQDVYDKLVPPFKQVIT 427

QY 315 GPADLKHDFDEFTQEAWS 332

DB 428 SETDTRYFDEBTAQTIT 445

RESULT 5

JC4345

protein kinase (EC 2.7.1.37) akt3 [validated] - rat

N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004

C;Accession: JC4345

R;Koniishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K

Biochem. Biophys. Res. Commun. 216, 526-534, 1995

A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase

e C subpecies and beta gamma subunits of G proteins.

A;Reference number: JC4345; MUID: 96063640; PMID: 7488143

A;Accession: JC4345

A;Molecule type: mRNA

A;Residues: 1-454 <KON>

A;Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DDBJ:D49836; NID:g1136777; PI

A;Experimental source: brain

C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A;Pathway: signal transduction pathways regulating various processes

C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F;4-105/Domain: pleckstrin repeat homology <PLK>

F;146-405/Domain: protein kinase homology <KIN>

F;154-162/Region: protein kinase ATP-binding motif

F;177/Active site: Lys #status predicted

Query Match 43.8%; Score 858; DB 1; Length 454;

Best Local Similarity 51.6%; Pred. No. 1.4e-33;

Matches 164; Conservative 50; Mismatches 100; Indels 4; Gaps 3;

QY 18 GNINLGPSANPNARPT--DFDFLVKVGKNGYKVLAKRKSDGAFYAVKVLQKKSILKNK 75

DB 129 GEEEMDASTTHKKRTKNDPDLKLGKTFGKVLVREKASGYAMKILKEVIAKD 188

QY 76 EQNHMAERNVLLKNVRHPLVGLRYSFQPEKLYFVLDYVNGGELFFHLQRRRRFLEPR 135

DB 189 EVAHTLTESRV-LKNTRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLRSRVFSEDR 247

QY 136 ARFYTAEVASAGLYHSLNIIYRDLPENILLDCQGHVLTDFGLCKECVEPEETTTSTFC 195

DB 248 TRFYGABIVSALDYLHSGKIVYRDLEKLENMLDKDGHKITDFGLCKEGITDAATMTKTC 307

QY 196 GTPPYLAPEVLKPEPYDRAVDWMLGAVLYEMHLGLPFFNTDVAQMYENILHQPQLQIPG 255

DB 308 GTPPYLAPEVLEDNDYGRAVDWMLGAVLYEMHCGRLPFFYNQDHEKLFELIMEDIKPPR 367

QY 256 GRTVAACDLLOGLLHKDQORL-GSKEDFLDKNHHMFSPINWDDLHYKRLTPPFPNVE 314

DB 368 TLSSDAKSLSLGLLIKDPNKRLLGGPDPAKEIMRHSFFSGVNWQDVYDKLVPPFKQVIT 427

QY 315 GPADLKHDFDEFTQEAWS 332

DB 428 SETDTRYFDEBTAQTIT 445

RESULT 6

S33364

protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse

N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004

C;Accession: S33364

R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner,

Oncogene 8, 745-754, 1993

A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt

A;Reference number: S33364; MUID: 93173519; PMID: 8437858

A;Accession: S33364

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-480 <BEL>

A;Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PI

C;Genetics:

A;Gene: MGI:Akt

A;Cross-references: MGI:87986

A;Map position: 12

C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni

A;Pathway: signal transduction pathways regulating various processes

C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen

F;4-106/Domain: pleckstrin repeat homology <PLK>

F;148-408/Domain: protein kinase homology <KIN>

F;156-164/Region: protein kinase ATP-binding motif

F;179/Active site: Lys #status predicted

F;308/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predict

F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 43.5%; Score 851.5; DB 1; Length 480;

Best Local Similarity 48.8%; Pred. No. 2.9e-33;

Matches 175; Conservative 55; Mismatches 115; Indels 15; Gaps 7;

QY 7 GVSPQPSRANGINILGPSANPNARPT--DFDFLVKVGKNGYKVLAKRKSDGAFYAVK 64

DB 123 GSPSDNSGABEVEVSL--AKPHRVTMNEFEVLKLGKTFGKVLVREKATGRYYAMK 179

QY 65 VLQKKSILKNKQNHMAERNVLLKNVRHPLVGLRYSFQPEKLYFVLDYVNGGELFFH 124

DB 180 ILKKEVIVAKDEVAHTLSE-NRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFH 238

QY 125 LOERRRFLPRARFYTAEVASAGLYHSL-LNIIYRDLPENILLDCQGHVLTDFGLCKE 183

DB 239 LGRERVFSFSDRARFYGAETVSALDYLHSEKVVYVYRDLEKLENMLDKDGHKIKITDFGLCKE 298

QY 184 CVEPEETTTTCCTPEYLAPEVLKPEPYDRAVDWMLGAVLYEMHLGLPFFNTDVAQMY 243

DB 299 GIKDGAATMTKTCGTPPYLAPEVLEDNDYGRAVDWMLGAVLYEMHCGRLPFFYNQDHEKLF 358

QY 244 ENILHQPQLQIPGRTVAACDLLOGLLHKDQORL-GSKEDFLDKNHHMFSPINWDDLHY 302

DB 359 ELILMBEIRFPRTGLGPEAKSLLSGLLKKDQPTQLRGLGGSEDAKEIMQHRFPANIVWQDVYE 418

QY	303	KRLTPFPNVEGPADLKHDPDFTQEAIVSKSGTCTPDTVASSSGASSA-----FLGFSYA 358	
Db	419	KKLSPPFKQVTSSETDTRYDFDEFTAQMITIT---PPQDDSMCECVDSRRRPHFPQFSYS 475	
RESULT 7			
A40831			
gag-akt polypeptide - AKT8 murine leukemia virus			
N;Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin			
C;Species: AKT8 murine leukemia virus			
C;Date: 12-Feb-1993 #sequence_revision 12-May-1994 #text_change 31-Dec-2004			
C;Accession: A40831; B40831			
R;Bellacosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.			
Science 254, 274-277, 1991			
A;Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH			
A;Reference number: A40831; MUID:92022574; PMID:1833819			
A;Accession: A40831			
A;Molecule type: DNA			
A;Residues: 1-262 <BEL>			
A;Cross-references: UNIPARC:UPI0000172SAP; GB:M80675			
A;Accession: B40831			
A;Molecule type: DNA			
A;Residues: 262-763 <B82>			
A;Cross-references: UNIPARC:UPI00001725B0; GB:M80675			
C;Genetics:			
A;Gene: gag-akt			
C;Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferas			
F;1-129/Product: core protein p15 #status predicted <CP1>			
F;130-214/Product: inner coat protein p12 #status predicted <CP2>			
F;284-763/Product: kinase-related transforming protein akt #status predicted <AKT>			
F;287-389/Domain: pleckstrin repeat homology <PLK>			
F;431-691/Domain: protein kinase homology <KIN>			
F;439-447/Region: protein kinase ATP-binding motif			
F;25,337/Binding site: carboxylate (Asn) (covalent) #status predicted			
F;462/Active site: Lys #status predicted			
F;609/Binding site: Phosphate (Tyr) (covalent) #status predicted			
Query Match 43.5%; Score 851.5; DB 1; Length 763;			
Best Local Similarity 48.6%; Pred. No. 4.3e-33;			
Matches 175; Conservative 55; Mismatches 115; Indels 15; Gaps 7;			
QY	7	GVPSPQSRANGNINLGPSANPNARPT--DFDPLKVIKGNVGYKVLAKRKSDBGAYVAK 64	
Db	406	GPSDDSGABEAEVSL---AKPKHRTVMNEFEYLLKLGKTFGKVLVKEKATGRYYAK 462	
QY	65	VLOKSKILKNKEQNHMAERNVLLKNVRHPPFLVGLRYSFQTPKLYFVLVDYVNGGELFFH 124	
Db	463	ILKKEVIVAKDEVAHTLTE-NRVLQNSRHPPFLTALKYSFQTHDRLCFVMEYANGGELFFH 521	
QY	125	LQRRFLPRARFYTAEVASAIYGLHS-LNIYIYRLKPNILLDCQGHVLTDFGLCKE 183	
Db	522	LSRERVFSEDRARFYGAETVSALDYLSHSEKNVYVRLKLENMLDKDGHIKITDFGLCKE 581	
QY	184	CVEPEETTSFGCTPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPFPNTDVAQNY 243	
Db	582	GKDGATMTKTFCTGTPYLAPEVLEDDNDYGRAVDWVGLVGVVYEMMCGRLPFFYNQDHEKLP 641	
QY	244	ENILHPLQIPGRTVAACDLLOGLLHKDQORL-GSKEDFLDIKNHMFSPINWDLLYH 302	
Db	642	ELILMEIRFPRTLGPENKSLSLGLLKQDPTQLGGSEDAKEIMQHRFPANIVQDVYE 701	
QY	303	KRLTPFPNVEGPADLKHDPDFTQEAIVSKSGTCTPDTVASSSGASSA-----FLGFSYA 358	
Db	702	KKLSPPFKQVTSSETDTRYDFDEFTAQMITIT---PPQDDSMCECVDSRRRPHFPQFSYS 758	
RESULT 8			
A46288			
protein kinase (EC 2.7.1.37) akt2 - human			
N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protei			
C;Species: Homo sapiens (man)			
C;Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004			

C;Accession: A46288			
R;Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Teguchi, T.; Franke, T.F.; Hamilton, T.C.; ;			
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992			
A;Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/(t			
A;Reference number: A46288; MUID:93028445; PMID:1409633			
A;Accession: A46288			
A;Molecule type: mRNA			
A;Residues: 1-481 <CHE>			
A;Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M95936; NID:g178325; PIDN			
A;Note: sequence extracted from NCBI backbone (NCBIP:115859)			
C;Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.			
C;Genetics:			
A;Gene: GDB:AKT2			
A;Cross-references: GDB:135650; OMIM:164731			
A;Map position: 19q13.2-19q13.2			
C;Function:			
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonil			
A;Pathway: signal transduction pathways regulating various processes			
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein			
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein			
F;4-106/Domain: pleckstrin repeat homology <PLK>			
F;150-409/Domain: protein kinase homology <KIN>			
F;158-166/Region: protein kinase ATP-binding motif			
F;181/Active site: Lys #status predicted			
Query Match 43.4%; Score 851; DB 1; Length 481;			
Best Local Similarity 47.8%; Pred. No. 3.1e-33;			
Matches 170; Conservative 55; Mismatches 119; Indels 12; Gaps 5;			
QY	10	SPQSRANGNINLGPS-ANPNARPTDFPLKVIKGNVGYKVLAKRKSDBGAFVAVKVLQK 68	
Db	126	SPSDSSTTEEMVAVSKARAKVTMNDFDYLLKLGKTFGKVLVREKATGRYYAMKILRK 185	
QY	69	SKILKNKEQNHMAERNVLLKNVRHPPFLVGLRYSFQTPKLYFVLVDYVNGGELFFHLORE 128	
Db	186	EVIIAKDEVAHTVTSRV-LQNRHPELTALYAFQTHDRLCFVMEYANGGELFFHLSRE 244	
QY	129	RFLPRARFYTAEVASAIYGLHS-LNIYIYRLKPNILLDCQGHVLTDFGLCKECVEPE 188	
Db	245	RVTBERARFYGAETVSALDYLSHSDRVVYRDKLENMLDKDGHIKITDFGLCKEGISDG 304	
QY	189	ETTSTFCGTPPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPFPNTDVAQMYENILH 248	
Db	305	ATMTKTCGTPPEYLAPEVLEDDNDYGRAVDWVGLVGVVYEMMCGRLPFYNDQHERLFFELIM 364	
QY	249	QPLQIPGRTVAACDLLOGLLHKDQORL-GSKEDFLDIKNHMFSPINWDLYHKRLTP 307	
Db	365	BEIRFPRTLSPKASLLAGLLKKDPKQLGGGSPDAKEVMEHRFFLSINWQDVVQKKLLP 424	
QY	308	PNPVVEGPADLKHDPDFTQEAIVSKSGTCTPDTVASSSG-----ASSAFLGFSYA 358	
Db	425	PPKQVTSVDTRYDFDEFT---AQSTITPPDRYDSLSLLELDQRTHPQFSYS 476	
RESULT 9			
JC2437			
protein kinase (EC 2.7.1.37) akt1 [validated] - rat			
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protei			
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004			
C;Accession: JC2437			
R;Konishi, H.; Shimomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.			
Biochem. Biophys. Res. Commun. 205, 817-825, 1994			
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associati			
A;Reference number: JC2437; MUID:95091823; PMID:7999118			
A;Accession: JC2437			
A;Molecule type: mRNA			
A;Residues: 1-480 <KON>			
A;Cross-references: UNIPROT:P47196; UNIPARC:UPI000012E044; DDBJ:D30040; NID:g485402; PII			
A;Experimental source: testis			
C;Function:			
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonil			
A;Pathway: signal transduction pathways regulating various processes			

submitted to the EMBL Data Library, July 1991

A:Reference number: S20836
A:Accession: S20836
A:Molecule type: mRNA
A:Residues: 63-70, 'TPSSSAACGSLSSNAPMWRLLRSGGVDDNRHPDCGRPQ', 'EAGGGDGLPVCLTORQLRGRDDGV
A:Cross-references: UNIPARC:UPI00001725AC; EMBL: X61037
A:Note: this sequence has been revised in reference S24423
R:Alessi, D.R.; Andjolkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming
EMBO J. 15, 6541-6551, 1996
A:Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
A:Reference number: A64193; MUID: 97133284; PMID: 8978691
A:Contents: annotation; phosphorylation sites
R:Toker, A.; Newton, A.C.
J. Biol. Chem. 275, 8271-8274, 2000
A:Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical PD
A:Reference number: A64193; MUID: 20187529; PMID: 10722653
A:Contents: annotation; autophosphorylation site
C:Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidy1-3
nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.
C:Genetics:
A:Gene: GDB:AKT1; RAC; PKB
A:Cross-references: GDB:111989; OMIM:164730
A:Map position: 14q32.1-q32.32
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes including insulin a
a production

Query Match	Score	DB 1	Length
Best Local Similarity	48.3%	847.5	480
Matches 174	Conservative	Pred. No. 4.5e-33	
Matches 174	Conservative	56	Mismatches 115
			Indels 15
			Gaps 7

Qy	7	GVPSPQPSRANGNINILGSPANPNARP	T---D	DFLKVITCKGNYGKVLAKRKS	SDGAFYAVK	64		
Db	123	GPSDMSGAEEMVSL---	AKPGRVTVNNEFPEYKLLGKGF	GKGVILKVBKATGR	YAYAMK	179		
Qy	65	VLOKSILKNKEQHINHAERNVLLKNVR	HPFLVGLRYSFQTP	EKLIVFLDVYVNGEL	FFPH	124		
Db	180	ILKKEVIAKDEVAHTL	TE-NRVLQNSRHPFL	TALKYTSFQTHDRL	CFWMEYANGGEL	238		
Qy	125	LORRRFLRPARFYTA	EVAASAI GYLHS-LNII	YRDLKPENILLDCQ	GHVLTDFGLCKE	183		
Db	239	LSRERVTSRDFYGA	BIVSALDYLSHSEKNVVR	DLKLEMLDKDQGH	IKITDFGLCKE	298		
Qy	184	CVEPEETTSTFCGTP	PEVLAPEVLRAKEPY	DRAVDMWCLGAV	IYEMHLGULPFP	FNFTDVAQMY	243	
Db	299	GIKDGA	MTKTCFCTGTP	EVLAPEVL	EDNDYGRAVDMWGL	VWVYEMMCGRLPE	VNQDHEKLF	358
Qy	244	ENILHQPLQIPGGRT	VAACDLLOGLLHKDQ	RQRL-GSKED	FLDIKNHMFPS	INWDDLIYH	302	
Db	359	ELILMBEIRFPRT	LGPEAKSLLSGLL	KDKPKRQGGG	SEDAKEIMQHRFF	AGIVQWVHYE	418	
Qy	303	KRLTPPNPNVGE	PADLKHDPDETQ	EAUSKISGCTP	DTPVASSSGASSA	----	FLGFSYA	358
Db	419	KKLSPFPKFOVTS	DTDFYDFDEE	FTAO	MITIT---PPD	DSMECVDS	SRPHRPFORSYS	475

RESULT 12

protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: S62117; S24423; S17999; S15714; S36388
R;Coffier, P.J.; Woodgett, J.R.

submitted to the EMBL Data Library, December 1991

A;Reference number: S62117
A;Accession: S62117
A;Molecule type: mRNA
A;Residues: 1-480 <COF>
A;Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:g630; PIDN:
A;Note: this is a revision to the sequence from reference S17999
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A;Reference number: S24423; MUID:92249329; PMID:1533586
A;Contents: erratum
A;Accession: S24423
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 70-78, 'N', 80-145 <CON>
A;Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036
R;Note: this is a revision to the sequence from reference S17999
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kina
A;Reference number: S17999; MUID:92037600; PMID:1718748
A;Accession: S17999
A;Molecule type: mRNA
A;Residues: 1-70, 'TPSSAACSGPRSSARSTWRPRSGVDHRHPDGGRRQAQAGGGDGLPVLITRRELGGRDGGVAGQ
A;Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036
R;Note: this sequence has been revised in references S62117 and S24423
C;Function:

Query Match 43.2%; Score 845.5; DB 1; Length 480;
Best Local Similarity 48.3%; Pred. No. 5.6e-33;
Matches 173; Conservative 58; Mismatches 114; Indels 13

Qy	10	SPOQSRANGINILGPS--ANPNARPT--DFFDLKVIUGKNYGVILLAKKSDCAFAVAKVL	66
Db	122	SGSPGSEAGABEVLAKPKHRTVMEFEYVLLKLGTFGKVLIVLKEKATAAYVAMKLL	181
Qy	67	QKSLKXNKQNHIMARNVLLKNVRHPFLVGLRYSFQTPBKLYEVLVYVNGGEFFHLQ	126
Db	182	KKEVIVAKDEVAHTLTE--NRVLQNSRHPSLTALXYSFQTHDRLCFVMEVANGGEFFHLS	240
Qy	127	RERRFLEPRARFYTAEVASALGYLHS--LNIIYRDLKPNILLDCOHVVLTDFGLCKEVC	185
Db	241	RERVSSDRARFYGAETVSDALYLSHSEKVVYRDLKLENMLDKDGHKITDFGLCKEGI	300
Qy	186	EPBETTSFCGCTPEYLAPEVLRKEPPYDRAVDWMCILGAVLYEMLHGLPFPFNTDVAQMYEN	245
Db	301	KDGAATMKTFCGCTPEYLAPEVLEDNDYGRAVDWVGVMYEMMCGRLFPYNDHEKLPFL	360
Qy	246	ILHQPLQIPCGRTVAACDLLOGLLHKQORL--GSKEDFLDKNHMFSPINWDDLYHKR	304
Db	361	ILMBEIRFPRTLSPKASKLSLGLLKQPKQRLGGSEDAKEIMQHRFFASIVWQDYEEK	420
Qy	305	LTPFPNPNVGPADLKHDFDEFTQAEVSKSIGCTPDTVASSSGASSA----FLGFSYA	358
Db	421	LSPPKPOVTSSETDTRVDFDEFTAOIMTIT---PPDOBDSMEGVDSRRPHPQPSYS	475

RESULT 13

protein kinase [EC 2.7.1.37] akt2 [validated] - rat
 N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Mar-2001 #sequence revision 31-Mar-2001 #text change 16-Aug-2004

C;Accession: JC2438
R;Koniishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association
A;Reference number: JC2437; MUID:95091823; PMID:7999118
A;Accession: JC2438
A;Molecule type: mRNA
A;Residues: 1-481 <KON>
A;Cross-references: UNIPROT:P47197; UNIPARC:UPI000012577E; DDBJ:D30041; NID:9485404; PID
A;Experimental source: testis
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes including myoblast
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;150-409/Domain: protein kinase homology <PK>
F;158-166/Region: protein kinase ATP-binding motif
F;181/Active site: Lys #status predicted

Query Match 42.7%; Score 837; DB 1; Length 481;
Best Local Similarity 47.2%; Pred. No. 1.4e-32;
Matches 168; Conservative 57; Mismatches 119; Indels 12; Gaps 5;

QY 10 SPOPSRANGNINLGPS-ANNPAPRTDPLKVTGKNGYGVLLAKRSDGAFYAVKVLQK 68
DB 126 SPDSSTSEMMVEAVSKARAKVTWMDPYLLKLGKGTGKVLVREKATGRYAMKILRK 185

QY 69 KSLKKNQNHMAERNVLLKNVHPFLVGLRYSFQTPPEKLYFVLDVYNGGELFFHLORE 128
DB 186 EVIADKDEVAHTVESRV-LQNRHPLTALKYAFQPHDLRCFVMEYANGDGLFFHLSRE 244

QY 129 RRFLEPRARYTAEVASAIYGLHSLNIIYRDLKPEINLLDCQGHVLTDFGLCKECVEPE 188
DB 245 RVFTEDRARYGAEIVSALYSLHSTDVVYRDIKLENMLDKDHIKITDFGLSKGISDG 304

QY 189 ETTSTFCGTPEYLAPVLRKEPYDRVDMWCLGAVLYEMLHGLPPFNPTDVAQMYENILH 248
DB 305 ATKTKTCGTPEYLAPVLRKEPYDRVDMWCLGAVLYEMLHGLPPFNPTDVAQMYENILH 364

QY 249 QPLQIPGRTVACDILGLLHKDQORQL-GSKEDFLDIKNHMFSPINWDDLIYHKLTP 307
DB 365 EIRFPRTLGPEAKSLLAGLLKKDKPQRLGGSPSDAKEVMEHFRFFISINQDVVQKLLP 424

QY 308 PFNPVNEGPADLKHDFEPTQEAIVSKSIGCTPTDVASSSGA-----SSAFLGFSYA 358
DB 425 PFKPQVTSEVDTRYDFDEFT-----AQSIITPDRVDSLGSLDQRTHPQFSYS 476

RESULT 14
A38578
protein kinase 2 (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 31-Dec-2004
C;Accession: A38578
R;Haribabu, B.; Dottin, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum
A;Reference number: A38578; MUID:91142122; PMID:1996312
A;Accession: A38578
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-479 <HAR>
A;Cross-references: UNIPROT:P28178; UNIPARC:UPI0000131B58; GB:M59744; NID:9167717; PIDN:
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin
F;151-407/Domain: protein kinase homology <KIN>
F;159-167/Region: protein kinase ATP-binding motif

Query Match 42.6%; Score 834; DB 2; Length 479;
Best Local Similarity 46.3%; Pred. No. 1.9e-32;
Matches 167; Conservative 65; Mismatches 115; Indels 14; Gaps 5;

QY 10 SPOPSRANGNINLGPSANP-----NARPTDFLKVIGKNGYGVLLAKRSDGA 59

DB 118 SPDSPNGSGNDDDEGEPEEVIFSKNQSATKDDPELLNVIGKSGFGKQVKKKGEDK 177
QY 60 FYAVKVLQKSKILKNKEQNHMAERNVLLKNVHPFLVGLRYSFQTPPEKLYFVLDVYNGG 119
DB 178 IFAMKVLRKDAIIRAKQVNHKSEKTI-LQCISHPPFIVNLHYAFQTKOKLYMVLDFVNGG 236
QY 120 ELFFHLQRRRRFLPRARFYTAEVASAIYGLHSLNIIYRDLKPEINLLDCQGHVLTDFG 179
DB 237 ELFFHLKREGRFSEPRVKIYAAIVSALDHLHKQDIVYRDLKPEINLLDSEGHICITDFG 296
QY 180 LKCEVPEBETSTFCGTPEYLAPVLRKEPYDRVDMWCLGAVLYEMLHGLPPFNPTDV 239
DB 297 LSKK-IETTDGTFTCGTPEYLAPVLRKEPYDRVDMWCLGAVLYEMLHGLPPFNPTDV 355
QY 240 AQMYENILHGLPQIPGRTVACDILGLLHKDQORQLGSKEDFLDIKNHMFSPINWDD 299
DB 356 STWIKLNGELKIPYIISPEAKSLLEGLLTREVDKRLGKGG-EYKQHPWFKNIDWEK 414
QY 300 LVHKRLTPFPNPNVEGPADLKHDFEPTQEAIVSKSIGCTPTDVASSSGASSAFLGFSYAQ 359
DB 415 LDRKEVEVHPKPKVSGTDSIQIDPVFTQERPMDSLVET-SALGDANGKDTSEGTYYA 473
QY 360 D 360
DB 474 D 474

RESULT 15
JS0178
protein kinase YKR2 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YMR104c; protein YMR104c
C;Species: Saccharomyces cerevisiae
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Oct-2004
C;Accession: JS0178; S30904; S54565
R;Kubo, K.; Ohno, S.; Matsumoto, S.; Yahara, I.; Suzuki, K.
Gene 76, 177-180, 1989
A;Title: A novel yeast gene coding for a putative protein kinase.
A;Reference number: JS0178; MUID:89306654; PMID:2663649
A;Accession: JS0178
A;Molecule type: DNA
A;Residues: 1-677 <KUB>
A;Cross-references: UNIPROT:P18961; UNIPARC:UPI000013BDFF; EMBL:M24929; NID:9295680; PI:
R;Chen, P.; Lee, K.S.; Levin, D.E.
Mol. Gen. Genet. 236, 443-447, 1993
A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell g
A;Reference number: S30903; MUID:93173125; PMID:8437590
A;Accession: S30904
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-677 <CHE>
A;Cross-references: UNIPARC:UPI000013BDFF
R;Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54510
A;Accession: S54565
A;Molecule type: DNA
A;Residues: 1-677 <HUN>
A;Cross-references: UNIPARC:UPI000013BDFF; EMBL:Z49702; NID:9817859; PIDN:CAA89740.1; P
A;Experimental source: strain AB972
C;Genetics:
A;Gene: SGD:YPK2; YKR2
A;Cross-references: SGD:S0004710; MIPS:YMR104C
A;Map position: 13R
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;35-57/Region: histidine-rich
F;342-599/Domain: protein kinase homology <KIN>
F;350-358/Region: protein kinase ATP-binding motif
F;351-375/Region: ATP binding #status predicted
F;466-512/Region: catalytic #status predicted

Query Match 42.5%; Score 833; DB 2; Length 677;
Best Local Similarity 49.4%; Pred. No. 2.9e-32;

Matches		174;	Conservative	52;	Mismatches	114;	Indels	12;	Gaps	6;
Qy	15	RANGNINL----GPSANPNARPTDFDLKVGKNGYKVLAKRKS DGA FYAVKVLQKKS 70								
Db	320	RGYGLNITVDYKPSKNKPLSIDDFDLKVGKSGKVMQVRKDTQKIYALKAR KAY 379								
Qy	71	ILKNKEQNHI MAERNVLLKNVRHPFLVGLRYSQTPKELYFVLVDYNGGELPFHLQERR 130								
Db	380	IVSKCEVTHTLAERTVLAR-VDCPFIVPLKFSQSPKELYLVLA FINGGELFYHLQHEGR 438								
Qy	131	FLEPRARFYTAEVASAI GYLHSNIIVRDLKPENILLDCQGHVVLTD FGLCKECVEPEET 190								
Db	439	FSLARSRFYIAELCALDSLHKL DVIYRDLKPENILLDYQGHIALCDFGLCKLNMKDNDK 498								
Qy	191	TSTFCGTPEYLAPEVL RKEPYDRAVDWMC LGAVLYEMLHGLPFPFNTDVAQMYENILHQP 250								
Db	499	TDTFCGTPEYLAPEILLGQGYTKTV DWTILGILLYEMMTGLPPYDENVVMYKILQQP 558								
Qy	251	LQIPGGRTVNACD LLOGLLHKDORQLG-SKEDFLDIKNHMPFSPINWDDL YHKRLTPPF 309								
Db	559	LLFPDGFDPAAKDLLIGLJSRDP SRRLGNGTD--EIRNHPFKDISWKLL LKGYIPPY 616								
Qy	310	NPNVGEPADLKHFDPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAQDD 361								
Db	617	KPIVKSEIDTANFDQBFTKE--KPIDSVVDEYLSAS-IQKQFGGWTYIGDE 664								

Search completed: January 27, 2006, 23:32:04
Job time : 11.8484 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:08:15 ; Search time 59.7818 Seconds
(without alignments)
4331.236 Million cell updates/sec

Title: US-09-868-131A-3

Perfect score: 1959

Sequence: 1 MASSPVGVPSPQSPRANGNI.....ASSAFLGFSYAQDDDDILDS 367

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1959	100.0	367	1	SGK2 MOUSE
2	1848	94.3	427	1	SGK2 HUMAN
3	1848	94.3	427	2	Q5H8Y6_HUMAN
4	1846	94.2	367	2	Q5R029_PONPY
5	1841	94.0	367	2	Q5T2R3_HUMAN
6	1837	93.8	393	2	Q52PK5_HUMAN
7	1832.5	93.5	366	2	Q5H8Z1_HUMAN
8	1615	82.4	302	1	SGK2 RAT
9	1427.5	72.9	350	2	Q4S7Y9_TETNG
10	1423	72.6	285	2	Q5H8Y4_HUMAN
11	1409	71.9	433	2	Q7ZTW4_BRARE
12	1403	71.6	431	2	Q5Q0U5_FUNHE
13	1397	71.3	432	2	Q6U1I9_CHICK
14	1392	71.1	434	2	Q93524_XENLA
15	1391	71.0	418	2	Q5BKX4_XENTR
16	1391	71.0	431	1	SGK1 RABIT
17	1389	70.9	431	2	Q68G05_RAT
18	1389	70.9	434	2	Q6GNB6_XENLA
19	1387	70.8	421	2	Q5TCN4_HUMAN
20	1387	70.8	431	2	Q5TCN3_HUMAN
21	1387	70.8	445	2	Q5TCN2_HUMAN
22	1387	70.8	526	2	Q5V765_HUMAN
23	1385.5	70.7	490	2	Q4RR91_TETNG
24	1385	70.7	431	1	SGK1 MOUSE
25	1385	70.7	519	2	Q6NS85_MOUSE
26	1383	70.6	431	1	SGK1 HUMAN
27	1382	70.5	431	2	Q4R633_MACFA
28	1381.5	70.5	594	2	Q73927_SQUNC
29	1380.5	70.5	430	1	SGK1 RAT
30	1377.5	70.3	433	2	Q73926_SQUNC
31	1372	70.0	434	2	Q6GLY8_XENLA

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32 1305.5 66.6 429 2 Q8VEK1_MOUSE
33 1305.5 66.6 496 1 SGK3_MOUSE
34 1299.5 66.3 518 2 Q4SFC2_TETNG
35 1297.5 66.2 429 2 Q6FHV7_HUMAN
36 1297.5 66.2 496 1 SGK3_HUMAN
37 1297.5 66.2 496 2 Q53EW6_HUMAN
38 1297.5 66.2 496 2 Q5R7A7_PONPY
39 1292.5 66.0 496 2 Q5H9Q5_HUMAN
40 1287.5 65.7 490 2 Q5ZJQ4_CHICK
41 1186 60.5 1114 2 Q4SYX7_TETNG
42 1034 52.8 316 2 Q4RI65_TETNG
43 1013 51.7 1550 2 Q4SYH0_TETNG
44 982 50.1 423 2 Q613H2_CAEBR
45 981 50.1 422 2 Q94365_CAEBL

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ALIGNMENTS

RESULT 1

SGK2_MOUSE STANDARD; PRT; 367 AA.

AC Q9QZS5; Q8R0P6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2).
GN Name=Sgk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagahisaka T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovskiy N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zvolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Iehi Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield C., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in the activation of potassium channels (By
similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9QZS5-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9QZS5-2; Sequence=YSP_004933;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: Not regulated by serum or glucocorticoids.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR ENBL; AFI69033; AAF12756.1; -; mRNA.
DR ENBL; AK050009; BAC34031.1; -; mRNA.
DR ENBL; BC026549; AAH26549.1; -; mRNA.
DR HSSP; P31751; IGZK.
DR Ensembl; ENSMUSG0000017868; Mus musculus.
DR MGI; MGI:1351318; Sgk2.
DR GO; GO:0015459; F:potassium channel regulator activity; ISS.
DR GO; GO:0004682; F:protein kinase Ck2 activity; ISS.
DR GO; GO:0017080; F:sodium channel regulator activity; ISS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; transferase.
FT DOMAIN 35 292 Protein kinase.
FT NP_BIND 41 49 ATP (By similarity).
FT MOTIF 68 78 Nuclear localization signal (By
similarity).
FT ACT_SITE 159 159 Proton acceptor (By similarity).

FT BINDING 64 64 ATP (By similarity).
FT MOD_RES 193 193 Phosphothreonine (by PDPK1) (By
similarity).
FT VARSP_LIC 171 199 Missing (in isoform 2).
FT CONFLICT 77 77 /FTID=VSP_004933.
FT CONFLICT 77 77 Missing (in Ref. 3).
SQ SEQUENCE 367 AA; 41359 MW; 668C04B1A1E9E33A CRC64;

Query Match 100.0%; Score 1959; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 5e-130;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSPVGVPSPOPSRANGNINLGPANPNARPTDFELKVIKGNVGVKLLAKRKS DGAF 60
Db 1 MASSPVGVPSPOPSRANGNINLGPANPNARPTDFELKVIKGNVGVKLLAKRKS DGAF 60

QY 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120
Db 61 YAVKVLQKKSILKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120

QY 121 LFFHLQRRRRFLPRARFYTAESAIGYLHSLNIYYRDLKPEINILLDCQGHVLTDFGL 180
Db 121 LFFHLQRRRRFLPRARFYTAESAIGYLHSLNIYYRDLKPEINILLDCQGHVLTDFGL 180

QY 181 CKECVEPEPTTSTFCGTPPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFNTDVA 240
Db 181 CKECVEPEPTTSTFCGTPPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFNTDVA 240

QY 241 QMYENILHQPLOIPGRTVAACDLLOGLLHKDOROLGSKEDFLDIKNHMFSPINWDDL 300
Db 241 QMYENILHQPLOIPGRTVAACDLLOGLLHKDOROLGSKEDFLDIKNHMFSPINWDDL 300

QY 301 YHKRLTPPPNPNVEGPADLKHFDPEFTQEA VSKSGICTPDTVASSSGASSAFILGFSYAQD 360
Db 301 YHKRLTPPPNPNVEGPADLKHFDPEFTQEA VSKSGICTPDTVASSSGASSAFILGFSYAQD 360

QY 361 DDDIILDS 367
Db 361 DDDIILDS 367

RESULT 2
SGK2_HUMAN
ID SGK2_HUMAN STANDARD; PRT; 427 AA.
AC Q9HBY8; Q9UKG6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2).
GN Name=SGK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), PHOSPHORYLATION SITE THR-253,
RP AND MUTAGENESIS OF SER-416.
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021.3440189;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.P., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehesvahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Stuce C.D., Smyth M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Scamaroni N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX TISSUE=Brain, and Colon;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION.
RX MEDLINE=22284526; PubMed=12397388; DOI=10.1007/s00424-002-0873-2;
RA Gamber N., Fillon S., Feng Y., Friedrich B., Lang P.A., Henke G.,
RA Huber S.M., Kobayashi T., Cohen P., Lang F.;
RT "K(+) channel activation by all three isoforms of serum- and
RT glucocorticoid-dependent protein kinase SGK.";
RL Pflugers Arch. 445:60-66(2002).
CC -|- FUNCTION: Involved in the activation of potassium channels.
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Names=2; Synonyms=beta;
CC IsoId=Q9HBY8-1; Sequence=Displayed;
CC Names=1; Synonyms=alpha;
CC IsoId=Q9HBY8-2; Sequence=VSP_004932;
CC -|- TISSUE SPECIFICITY: Highly expressed in liver, kidney and
CC pancreas, and at lower levels in brain.
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -|- CAUTION: Not regulated by serum or glucocorticoids.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF186470; AAG17012.1; -; mRNA.

DR EMBL; AF169034; AAF12757.2; -; mRNA.
DR EMBL; Z98752; CAC18509.1; -; Genomic DNA.
DR EMBL; BC014037; AAH14037.2; ALT SEQ; mRNA.
DR EMBL; BC065511; AAH65511.1; -; mRNA.
DR HSSP; P31751; IGZK.
DR Ensembl; ENSG00000101049; Homo sapiens.
DR HGNC; HGNC:13900; SGK2.
DR MIM; 607589; -.
DR GO; GO:0015459; Fipocassium channel regulator activity; IDA.
DR GO; GO:0004682; Fiprotein kinase CK2 activity; NAS.
DR GO; GO:0004674; Fiprotein serine/threonine kinase activity; TAS.
DR GO; GO:0017080; Fiprotein channel regulator activity; NAS.
DR GO; GO:0006468; Piprotein amino acid phosphorylation; TAS.
DR GO; GO:0007243; Piprotein kinase cascade; TAS.
DR GO; GO:0006979; Presponse to oxidative stress; TAS.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S-TK_X; 1.
DR SMART; SM00220; S-TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 95 352 Protein kinase.
FT NP_BIND 101 109 ATP (By similarity).
FT MOTIF 128 138 Nuclear localization signal (By similarity).
FT ACT_SITE 219 219 Proton acceptor (By similarity).
FT BINDING 124 124 ATP (By similarity).
FT MOD_RES 253 253 Phosphothreonine (by PDPK1).
FT VARSPLOC 1 60 Missing (in isoform 1).
FT MUTAGEN 416 416 S->D: Increased activation.
FT SEQUENCE 427 AA; 47604 MW; D8F0FAGDF54B1370 CRC64;
Query Match 94.3%; Score 1848; DB 1; Length 427;
Best Local Similarity 94.3%; Pred. No. 4.1e-122;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 MASSPVGVSPQPSRANGINLGPSANPNARPTDFLKVIGKNGYKVLAKRKSQDAP 60
DB 61 MNSSPAGTSPQPSRANGINLGPSANPNARPTDFLKVIGKNGYKVLAKRKSQDAP 120
QY 61 YAVKVLQKSLKKNKQSHIMAERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLVDYNGGE 120
DB 121 YAVKVLQKSLKKNKQSHIMAERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLVDYNGGE 180
QY 121 LFFHLQRRERFLPRARFYTAEVASAIQYLHLSNIIYRDLKPNILLDCQGHVLTDFGL 180
DB 181 LFFHLQRRERFLPRARFYTAEVASAIQYLHLSNIIYRDLKPNILLDCQGHVLTDFGL 240
QY 181 CKECVEPEETTSTFCGTPPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240
DB 241 CKECVEPEETTSTFCGTPPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFFSQDVS 300
QY 241 QMVENILHQPLOTGGRTVAACDLLOGLAHKQORQLSGKDFLDLKNHMFSPINWDDL 300
DB 301 QMVENILHQPLOTGGRTVAACDLLOGLAHKQORQLSGKDFLDLKNHMFSPINWDDL 360
QY 301 YHKRLTPPPNPVNEGVPADLKHFDPEFTQBAVSKSIGCTPDTVASSGSSAFLGFSYAQD 360
DB 361 YHKRLTPPPNPVNEGVPADLKHFDPEFTQBAVSKSIGCTPDTVASSGSSAFLGFSYAPE 420
QY 361 DDILD 366
DB 421 DDILD 426

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RESULT 3
Q5H8Y6 HUMAN
ID Q5H8Y6_HUMAN PRELIMINARY; PRT; 427 AA.
AC Q5H8Y6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE OTTHUMP0000031703.
GN Names=SGK2; ORFNames=RP1-138B7.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z98752; CAI42312.1; -: Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 427 AA; 47604 MW; D6F0F6ADF54B1370 CRC64;

Query Match 94.3%; Score 1848; DB 2; Length 427;
Best Local Similarity 94.3%; Pred. No. 4.1e-122;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVKLLAKRSDGAF 60
DB 61 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVKLLAKRSDGAF 120
QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120
DB 121 YAVKVLQKKSILKNKEQHMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 180
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
DB 181 LFFHLQRRERFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240
QY 181 CKCEVEPEPTTSTFCGTPPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVA 240
DB 241 CKEGVEPEPTTSTFCGTPPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMLHGLPPFFYSQDVS 300
QY 241 QMYENILHQPLOIPGGRVTAACDLQLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
DB 301 QMYENILHQPLOIPGGRVTAACDLQLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 360
QY 301 YHKRLTPFPNPNVVEGPAADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
DB 361 YHKRLTPFPNPNVGTGPAADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
QY 361 DDILD 366
DB 421 DDILD 426

RESULT 4
Q5RDZ9_PONPY PRELIMINARY; PRT; 367 AA.
AC Q5RDZ9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp469N2435.
GN Name=DKFZp469N2435;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA The German cDNA Consortium;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857741; CAH90008.1; -: mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Hypothetical protein.
SQ SEQUENCE 367 AA; 41218 MW; 61128B6CC0519B73 CRC64;

Query Match 94.2%; Score 1846; DB 2; Length 367;
Best Local Similarity 94.3%; Pred. No. 4.7e-122;
Matches 345; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVKLLAKRSDGAF 60
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFDLKVIKGNVGVKLLAKRSDGTF 60
QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120
DB 61 YAVKVLQKKSILKNKEQHMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
QY 181 CKCEVEPEPTTSTFCGTPPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVA 240
DB 181 CKEGVEPEPTTSTFCGTPPEYLAPEVLKPEYDRAVDWVWCLGAVLYEMLHGLPPFFYSQDVS 240
QY 241 QMYENILHQPLOIPGGRVTAACDLQLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
DB 241 QMYENILHQPLOIPGGRVTAACDLQLLHKDQRLGSKEDFLDIKNHMFSPINWDDL 300
QY 301 YHKRLTPFPNPNVVEGPAADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAQD 360
DB 301 YHKRLTPFPNPNVAGPADLKHFDPFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 361 DDILD 366
DB 361 DDILD 366
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RESULT 5
Q52R3 HUMAN
AC Q52R3
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Serum/glucocorticoid regulated kinase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR GO: 0005524; F:ATP binding; IEA.
DR GO: 0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: 0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase_1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; Tyr_K; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ
Sequence 367 AA; 41233 MW; C91DD892C4C2486B CRC64;

Query Match 94.0%; Score 1841; DB 2; Length 367;
Best Local Similarity 94.0%; Pred. No. 1.1e-121;
Matches 344; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGINILGPSANPNARPTDFDLKVLKGVKGYKVLAKRKSDFGAF 60
DB 1 MNSSPAGTTPSQPSRANGINILGPSANPNARPTDFDLKVLKGVKGYKVLAKRKSDFGAF 60

QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPLVGLRYSQTPEKLYFVLDYVNGGE 120
DB 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPLVGLRYSQTPEKLYFVLDYVNGGE 120

QY 121 LFFHLQRRERFLPRARFYAEVASAIGYLHLSNIIYRDLKPNILLDCQGHVLTDFGL 180
DB 121 LFFHLQRRERFLPRARFYAEVASAIGYLHLSNIIYRDLKPNILLDCQGHVLTDFGL 180

QY 181 CKECVPEPTTSTFCGTPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240
DB 181 CKECVPEPTTSTFCGTPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240

QY 241 QMVENILHQLPIPGGRTVAACDLQGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 300
DB 241 QMVENILHQLPIPGGRTVAACDLQGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 300

QY 301 YHKRLTPPPNPNVEGADLKHFDPEFTQEAIVSKSIGCTPDTVAASSGASSAFGLGFSYAQD 360
DB 301 YHKRLTPPPNPNVEGADLKHFDPEFTQEAIVSKSIGCTPDTVAASSGASSAFGLGFSYAQD 360

us-09-868-131a-3.rup
Q52PK5 HUMAN PRELIMINARY; PRT; 393 AA.
AC Q52PK5
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Serum/glucocorticoid regulated kinase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR GO: 0005524; F:ATP binding; IEA.
DR GO: 0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: 0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase_1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; Tyr_K; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ
Sequence 393 AA; 43962 MW; B9931E71A8B998D6 CRC64;

Query Match 93.8%; Score 1837; DB 2; Length 393;
Best Local Similarity 93.7%; Pred. No. 2.2e-121;
Matches 343; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGINILGPSANPNARPTDFDLKVLKGVKGYKVLAKRKSDFGAF 60
DB 27 MNSSPAGTTPSQPSRANGINILGPSANPNARPTDFDLKVLKGVKGYKVLAKRKSDFGAF 86

QY 61 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPLVGLRYSQTPEKLYFVLDYVNGGE 120
DB 87 YAVKVLQKKSILKNKEQHMAERNVLLKNVRHPLVGLRYSQTPEKLYFVLDYVNGGE 146

QY 121 LFFHLQRRERFLPRARFYAEVASAIGYLHLSNIIYRDLKPNILLDCQGHVLTDFGL 180
DB 147 LFFHLQRRERFLPRARFYAEVASAIGYLHLSNIIYRDLKPNILLDCQGHVLTDFGL 206

QY 181 CKECVPEPTTSTFCGTPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240
DB 207 CKECVPEPTTSTFCGTPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 266

QY 241 QMVENILHQLPIPGGRTVAACDLQGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 300
DB 267 QMVENILHQLPIPGGRTVAACDLQGLLHKDQRLGSKEDFLDIKNHFFSPINWDDL 326

QY 301 YHKRLTPPPNPNVEGADLKHFDPEFTQEAIVSKSIGCTPDTVAASSGASSAFGLGFSYAQD 360
DB 301 YHKRLTPPPNPNVEGADLKHFDPEFTQEAIVSKSIGCTPDTVAASSGASSAFGLGFSYAQD 360
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Db 327 YHRLTPPPNPNVTPADLKHDFEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAPE 366
QY 361 DDILD 366
Db 387 DDILD 392

RESULT 7
Q5H8Z1_HUMAN
ID Q5H8Z1_HUMAN PRELIMINARY; PRT; 366 AA.
AC Q5H8Z1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE OTHUMP00000031706.
GN Name=SGK2; ORFNames=RPI-138B7.2-006;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z98752; CAI42315.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 366 AA; 41047 MW; 8BB346894C23571F CRC64;

Query Match 93.5%; Score 1832.5; DB 2; Length 366;
Best Local Similarity 94.0%; Pred. No. 4.2e-121;
Matches 344; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

QY 1 MASSPVGVSPQSRANGINLGPSANPNARPTDFDLKVGKNGYGVLLAKRKS DGAF 60
Db 1 MNSSPAGTSPQSRANGINLGPSANPNARPTDFDLKVGKNGYGVLLAKRKS DGAF 60
QY 61 YAVKVLQKSLKKNKQNHIAERNVLLKNVRHPLVGLRYSFQTEKLYFVLVDYNGGE 120
Db 61 YAVKVLQKSLKKEE-SHIMAEKSVLLKNVRHPLVGLRYSFQTEKLYFVLVDYNGGE 119
QY 121 LFFHLQRRERFLEPRARFYTAEVASAIQYLHLSNIYYRDLKPEINILLDCQGHVLTDFGL 180
Db 120 LFFHLQRRERFLEPRARFYTAEVASAIQYLHLSNIYYRDLKPEINILLDCQGHVLTDFGL 179
QY 181 CKECVPEPTTSTFCGTPPEYLAPEVLRKGPYDRAVDWVCLGAVLYEMLHGLPPFFNTDVA 240
Db 180 CKEGVEPEDTSTFCGTPPEYLAPEVLRKGPYDRAVDWVCLGAVLYEMLHGLPPFFSQDVS 239
QY 241 QMYENILHQLPQIPGGRVTAACDLLOGLLHKQORQLGSKEDFLDIKNHMFSPINWDDL 300
Db 240 QMYENILHQLPQIPGGRVTAACDLLOGLLHKQORQLGSKADFLDIKNHVFSPINWDDL 299
QY 301 YHRLTPPPNPNVVEGADLKHDFEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAOD 360
Db 300 YHRLTPPPNPNVTPADLKHDFEFTQEA VSKSIGCTPDTVASSGASSAFLGFSYAPE 359
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QY 361 DDILD 366
Db 360 DDILD 365

RESULT 8
SGK2_RAT
ID SGK2_RAT STANDARD; PRT; 302 AA.
AC Q8RAU9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2) (Fragment).
GN Name=Sgk2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Feng Y.X.; Huber S.M.; Waerntges S.; Lang F.;
RT "SGK2 and SGK3 mRNA expression in rat kidney.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the activation of potassium channels (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL; AF361756; AAL91351.1; -; mRNA.
CC HSSP; F31751; IGZK.
CC DR Ensembl; ENSRNOG00000033573; Rattus norvegicus.
CC RGD; 620232; Sgk2.
CC DR GO; GO:0015459; F:potassium channel regulator activity; ISS.
CC DR GO; GO:0004682; F:protein kinase CK2 activity; ISS.
CC DR GO; GO:0017080; F:sodium channel regulator activity; ISS.
CC DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser_Thr_pkin_AS.
CC InterPro; IPR002290; Ser_Thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TK; 1.
CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
CC DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 18 275
FT NP_BIND 24 32
FT MOTIF 51 61
FT ATP (By similarity).
FT Nuclear localization signal (By similarity).
FT Proton acceptor (By similarity).
FT BINDING 47 47
FT MOD_RES 176 176
FT Phosphothreonine (by PDPK1) (By similarity).
FT
FT NON_TER 1 1
FT NON_TER 302 302
FT SEQUENCE 302 AA; 34622 MW; A74BE3F424283D66 CRC64;
SQ

Query Match 82.4%; Score 1615; DB 1; Length 302;
Best Local Similarity 99.3%; Pred. No. 7.3e-106;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

QY 18 GNINLGSANPNARPTDFDLKVGKGYGVLLAKRSDGAFYAVKVLQKKSILKNKEQ 77
 Db 1 GNINLGSANPNARPTDFDLKVGKGYGVLLAKRSDGAFYAVKVLQKKSILKNKEQ 60
 QY 78 NHIMAERNVLLKNVRHPLGLRYSFQTPPEKLYFVLVDYVNGGELFFHLQRRRFLPEPR 137
 Db 61 SHIMAERNVLLKNVRHPLGLRYSFQTPPEKLYFVLVDYVNGGELFFHLQRRRFLPEPR 120
 QY 138 FYTAEVASAIGYLHSLNIIRDLKPNILLDCQGHVVLTDGFLCKECVPEPETTTSTFCGT 197
 Db 121 FYTAEVASAIGYLHSLNIIRDLKPNILLDCQGHVVLTDGFLCKECVPEPETTTSTFCGT 180
 QY 198 PEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPGGR 257
 Db 181 PEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPGGR 240
 QY 258 TVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLYHKRLTTPFPNPNVEGPA 317
 Db 241 TVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLYHKRLTTPFPNPNVEGPA 300
 QY 318 DL 319
 Db 301 DL 302

RESULT 9
 Q4S7Y9 TETNG
 ID Q4S7Y9 TETNG PRELIMINARY; PRT; 350 AA.
 AC Q4S7Y9; 2005 (TEMBLrel. 31, Created)
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE Chromosome 9 SCAF14710, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG0022577001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasiiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wengner P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype".
 RL Nature 431:946-957 (2004).
 RN [2]

NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -i- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -i- FUNCTION: Plays a key role in the control of the eukaryotic cell
 CC cycle. It is required in higher cells for entry into S-phase and
 CC mitosis. Component of the kinase complex that phosphorylates the
 CC repetitive C-terminus of RNA polymerase II. Catalytic component of
 CC MPF (By similarity).
 CC -i- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
 CC mature oocytes (By similarity).
 CC -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; CAAE01014710; CAG03243.1; -; Genomic_DNA.
 DR InterPro; IPR000961; pkinase C.
 DR InterPro; IPR000719; prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase C.1.
 DR Pfam; PF00433; pkinase C.1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKG; 1.
 DR SMART; SM00219; TyrKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Nucleotide-Binding;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 350 AA; 39571 MW; 56BP9C5C2889D924 CRC64;

Query Match 72.9%; Score 1427.5; DB 2; Length 350;
 Best Local Similarity 75.7%; Pred.No. 1.5e-92;
 Matches 265; Conservative 37; Mismatches 47; Indels 1; Gaps 1;

QY 16 ANGNINLGSANPNARPTDFDLKVGKGYGVLLAKRSDGAFYAVKVLQKKSILKNK 75
 Db 2 SHDDVNLGFSANPHARPTDFDLAVIGKGTGKVLAKHTDSSFYAVKVLQKVKKK 61
 QY 76 EQNHMAERNVLLKNVRHPLGLRYSFQTPPEKLYFVLVDYVNGGELFFHLQRRRFLPEPR 135
 Db 62 EQKNIMAERNVLLKSLKHPFLVRLHYSFQTAELKLYFVLVDYVNGGELFFHLQRRRFLPEPR 121
 QY 136 AREYTAEVASATGYLHSLNIIRDLKPNILLDCQGHVVLTDGFLCKECVPEPETTTSTFC 195
 Db 122 ARPYAAEVASATGYLHSLNIIRDLKPNILLDCQGHVVLTDGFLCKECVPEPETTTSTFC 181
 QY 196 GTPEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPG 255
 Db 182 GTPEYLAPVLRKEPYDRIWCLGAVLYEMLHGLPPFFNTDVAQMYENILHQLQIPG 241
 QY 256 GRTVAACDLLOGLLHKDQRLGSKEDFLDIKNHMFPSINWDDLYHKRLTTPFPNPNVEG 315
 Db 242 GKSDAVCSLLVGLLQKQHRRLGAIADFLKHNHVFPTINWDDLYHKRLTTPFPNPNVGR 301
 QY 316 PADLKHFDPEFTQEAIVSKSIGCTPDTVASSSGASSAFGLGESYAQDDDL 365
 Db 302 PADTQHIDPEFTREVMVSSVSQTPEFTASAS-ASNAFNGFSFVATEDSFL 350

RESULT 10
 Q5H8Y4 HUMAN
 ID Q5H8Y4_HUMAN PRELIMINARY; PRT; 285 AA.
 AC Q5H8Y4;
 DT 10-MAY-2005 (TEMBLrel. 30, Created)
 DT 10-MAY-2005 (TEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TEMBLrel. 30, Last annotation update)
 DE OTTHUMP00000031704.
 GN Name=SGK2; ORFNames=RP1-138B7.2-004;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Beasley H.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; Z98752; CAI42314.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

```
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 285 AA; A3493A701ABB4542 CRC64;

Query Match 72.6%; Score 1423; DB 2; Length 285;
Best Local Similarity 94.0%; Pred. No. 2.4e-92;
Matches 267; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MASSPVGVSPQPSRANGINLGPSANPNARPTDFDLKVIKGNVGVLLAKRKSDGAF 60
DB 1 MNSSPAGTSPQPSRANGINLGPSANPNARPTDFDLKVIKGNVGVLLAKRKSDGAF 60

QY 61 YAVKVLQKKSILKKNQHIMAEARNVLLKNVRHPLVGLRYSFQTPEKLVFLVDYNGGE 120
DB 61 YAVKVLQKKSILKKNQHIMAEARNVLLKNVRHPLVGLRYSFQTPEKLVFLVDYNGGE 120

QY 121 LFPHLQRRRFLPRARFYTAEVAASIGVLSHLSNIYYRDLKPNILLDCQGHVLLDFGL 180
DB 121 LFPHLQRRRFLPRARFYTAEVAASIGVLSHLSNIYYRDLKPNILLDCQGHVLLDFGL 180

QY 181 KCEVPEETSTFCGTPEYLADEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVA 240
DB 181 KCEVPEETSTFCGTPEYLADEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVA 240

QY 241 QMYENILHQLPIPGGRTVAACDLLOGLLHKDQORLGSKEDEPL 284
DB 241 QMYENILHQLPIPGGRTVAACDLLOGLLHKDQORLGSKEDEPL 284

RESULT 11
O72TW4 BRARE
ID O72TW4 BRARE PRELIMINARY; PRT; 433 AA.
AC O72TW4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serum/glucocorticoid regulated kinase.
GN Name=sgk;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney, and Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udell T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Cunarstne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallick D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole body;
RG NIH MGC Project;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG NIH MGC Project;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and
CC monomeric catalytic subunit). Translocates into the nucleus
CC (monomeric catalytic subunit) (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC052134; AAH52134.1; -; mRNA.
DR EMBL; BC067618; AAH67618.1; -; mRNA.
DR HSP; P31751; IMRY.
DR Ensembl; ENSDARG0000025522; Danio rerio.
DR ZFIN; ZDB-GENE-030131-2860; sgk.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase; cAMP.
SQ SEQUENCE 433 AA; 48983 MW; F2AA4771E245FF56 CRC64;

Query Match 71.9%; Score 1409; DB 2; Length 433;
Best Local Similarity 72.5%; Pred. No. 3.8e-91;
Matches 261; Conservative 44; Mismatches 51; Indels 4; Gaps 2;

QY 9 PSPQPSRANGINLGPSANPNARPTDFDLKVIKGNVGVLLAKRKSDGAFYAVKVLQK 68
DB 75 PSPQPSQ-QINLGFSSNPTAKPSDFDLKVIKGSFGKVLARHRSDEKFAVAVKVLQK 133

QY 69 KSILKKNQHIMAEARNVLLKNVRHPLVGLRYSFQTPEKLVFLVDYNGGELFFHLQRE 128
DB 134 KAILKKKEKHMSEARNVLLKNVRHPLVGLRYSFQTPEKLVFLVDYNGGELFFHLQRE 193

QY 129 RFLEPRARFYTAEVAASIGVLSHLSNIYYRDLKPNILLDCQGHVLLDFGLCKEVEPE 188
DB 194 RCLEPRARFYTAEVAASIGVLSHLSNIYYRDLKPNILLDSQGHILTFDLCKENIEPN 253

QY 189 ETTSTFCGTPEYLADEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 248
DB 254 GTTSTFCGTPEYLADEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFNTDVAQMYENILH 313

QY 249 QPLQPGGRTVAACDLLOGLLHKDQORLGSKEDEFLDIKNHMFPSPINWDDLVHKLTPP 308
DB 314 KPLQKPNISNARHLLSGLLQKQTKRLGFTDDTFTEIKNMFPSPINWDDLVHKLTPP 373

QY 309 FNPVNPADLKHDFEFTQEAIVSKSIQCTPT---VASSGSAFAFLGFSYAQDDDDIL 365
DB 374 FNPVNTGPNLDRHDFEFTPEVPNSIGCSPDSALVTSITEATFLGFSYAPAMDVYL 433
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RESULT 12
Q5Q0U5_FUNHE PRELIMINARY; PRT; 431 AA.
ID AC Q5Q0U5_FUNHE
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serum and glucocorticoid-regulated kinase.
GN Name=SGK;
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OC NCBI_TaxID=8078;
RN [1]
RC NUCLEOTIDE SEQUENCE.
PC TISSUE=Liver;
RA Sato J.D., Clarke C.C., Stanton B.A.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY800243; AA080429.1; -; mRNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ
SEQUENCE 431 AA; 48870 MW; 91C80821F64B454D CRC64;

Query Match 71.6%; Score 1403; DB 2; Length 431;
Best Local Similarity 71.7%; Pred. No. 1e-90;
Matches 258; Conservative 47; Mismatches 51; Indels 4; Gaps 2;

QY 9 P5PQPSRANGINLGPSANPNARPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQK 68
DB 73 P5PQPSQ-QINLGPSNPSAKPSDFHLKLVIGKSGFGKVLARHRTDQFVAVKVLQK 131

QY 69 KSLKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGELFFHLORE 128
DB 132 KALKKKEKHIMSERVLLKNVKHPLVGLHYSFQTADKLYFVLDYINGGELFYHLORE 191

QY 129 RRFLEPRARYTAEVASAIYGLHSLNIYRDLKPNILLDCQGHVLTDFGLCKECVEPE 188
DB 192 RCFLEPRARYSAEIASALYGLHSLNIYRDLKPNILLDSQGHILTDFGLCKENIEPN 251

QY 189 ETTSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFTNTDVAQMYENILH 248
DB 252 GTTSTFCGTPEYLAPEVLRKEPYDRTVDMWCLGAVLYEMLYGLPPFSRNTAEYDNLN 311

QY 249 QPLQIPGGRVTAACDLLOGLLHKDQRLGSKEDFLDKNHMFPSPINWDDLHYKRLTTP 308
DB 312 KPLQLKPNITNSARHLEGLLQKDRTKRLGAKEDFTEIKNHVFPSPINWDDLNAKWTTP 371

QY 309 FNPVNEGADLKHFDPEFTQEAIVSKISGCTPD---TVASSSGASSAFLGFSYAQDDDDIL 365
DB 372 FNPVNTGPNLDRHFDPEFTDEPVSSIGCSFDALATASIKAAEAFVGFSPYSDSYL 431

RESULT 13
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Q6UI19_CHICK
ID AC Q6UI19_CHICK PRELIMINARY; PRT; 432 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Serum and glucocorticoid-induced kinase.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Malkiewicz S.A., Porter T.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY380825; AA088435.1; -; mRNA.
DR HSSP; P05132; IATP.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ
SEQUENCE 432 AA; 48890 MW; 83AB52AFF2609953 CRC64;

Query Match 71.3%; Score 1397; DB 2; Length 432;
Best Local Similarity 71.7%; Pred. No. 2.7e-90;
Matches 258; Conservative 49; Mismatches 49; Indels 4; Gaps 2;

QY 9 P5PQPSRANGINLGPSANPNARPTDFDLKLVIGKNGYKVLAKRSDGAFYAVKVLQK 68
DB 74 P5PQPSQ-QINLGPSNPHAKPSDFHLKLVIGKSGFGKVLARHAKESQFVAVKVLQK 132

QY 69 KSLKNKEQNHIAMERNVLLKNVRHPLVGLRYSFQTPEKLYFVLDYVNGGELFFHLORE 128
DB 133 KALKKKEKHIMSERVLLKNVKHPLVGLHYSFQTADKLYFVLDYINGGELFYHLORE 192

QY 129 RRFLEPRARYTAEVASAIYGLHSLNIYRDLKPNILLDCQGHVLTDFGLCKECVEPE 188
DB 193 RCFLEPRARYAEIASALYGLHSLNIYRDLKPNILLDSQGHIVLTDFGLCKENIEHN 252

QY 189 ETTSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFTNTDVAQMYENILH 248
DB 253 GTTSTFCGTPEYLAPEVLRKEPYDRTVDMWCLGAVLYEMLYGLPPFSRNTAEYDNLN 312

QY 249 QPLQIPGGRVTAACDLLOGLLHKDQRLGSKEDFLDKNHMFPSPINWDDLHYKRLTTP 308
DB 313 KPLQLKPNITNSARHLEGLLQKDRTKRLGAKEDFTEIKNHVFPSPINWDDLNAKWTTP 372

QY 309 FNPVNEGADLKHFDPEFTQEAIVSKISGCTPDTV---ASSSGASSAFLGFSYAQDDDDIL 365
DB 373 FNPVNSGPNLDRHFDPEFTDEPVNSIGQSPSILITASVKAAEAFVGFSPYSDSYL 432

RESULT 14
O93524_XENLA
ID AC O93524_XENLA PRELIMINARY; PRT; 434 AA.
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
```


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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:06:05 ; Search time 76.3566 Seconds
(without alignments)
2468.595 Million cell updates/sec

Title: US-09-868-131A-4
Perfect score: 2269
Sequence: 1 MALKIPAKRIFGNFDPDFI.....EADDAFGVGFYAPPSSEDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2269	100.0	429	3	AAY95278 Human ser
2	2269	100.0	429	7	Adn38798 Cancer/an
3	2269	100.0	429	9	ADY17700 PRO polyp
4	2269	100.0	436	4	AM40620 Human pol
5	2269	100.0	496	4	AAU87228 Novel cen
6	2269	100.0	496	4	AAU87382 Novel cen
7	2269	100.0	496	8	ADI54543 Novel hum
8	2269	100.0	496	8	ADI54697 Novel hum
9	2269	100.0	496	8	ADQ15046 Human can
10	2263	99.7	496	2	AAW87772 Human ser
11	2254	99.3	496	4	AAW38834 Human pol
12	2246	99.0	429	3	AB24114 Human ser
13	2246	99.0	496	8	ADRI4041 Human NF-
14	2061	90.8	397	9	ADY18746 PRO polyp
15	2061	90.8	464	4	AM33732 Human pol
16	2061	90.8	464	8	ADL31662 Human pro
17	1974	87.0	446	4	AA65616 Novel pro
18	1974	87.0	446	8	ADI29222 Human MAR
19	1699	74.9	322	4	AAW99837 AGC prote
20	1699	74.9	322	8	ADJ38885 SGK3 amin
21	1556.5	68.6	372	8	ABM33102 Human dia
22	1501	66.2	526	6	ADA54293 Human pro
23	1501	66.2	526	7	ADG31710 Human pro
24	1476	65.1	407	7	ADC69794 Human ser

25	1476	65.1	431	2	AAW90139 Human sgk
26	1476	65.1	431	3	AB24116 Rat serum
27	1476	65.1	431	3	AAY93530 A rat ser
28	1476	65.1	431	6	ADA10889 Human CDN
29	1476	65.1	431	6	ADG31708 Human pro
30	1476	65.1	431	7	ADK50982 Human NOV
31	1476	65.1	431	7	ADK50984 Human NOV
32	1476	65.1	431	8	ADK50984 Human NOV
33	1476	65.1	431	9	ADY14632 PRO polyp
34	1476	65.1	431	9	ADY19878 PRO polyp
35	1476	65.1	431	9	AEA04529 Human pro
36	1476	65.1	442	7	ADG31706 Human pro
37	1476	65.1	445	7	ADC69792 Human pro
38	1474.5	65.0	430	7	ADN95217 Human BEC
39	1472	64.9	431	7	AAW77217 Human cel
40	1472	64.9	431	3	AB24115 Human ser
41	1472	64.9	431	4	AB25613 Novel pro
42	1472	64.9	431	7	ADD14174 Human src
43	1472	64.9	431	7	ADK31655 Human 290
44	1472	64.9	431	8	ADI29219 Human MAR
45	1472	64.9	431	8	ADN03773 Antipsori

ALIGNMENTS

RESULT 1
AAY95278
ID AAY95278 standard; protein; 429 AA.
XX
AC AAY95278;
XX
DT 12-SEP-2000 (first entry)
XX
DE Human serum and glucocorticoid-induced protein kinase 3.
XX
KW Serum and glucocorticoid-induced protein kinase 3; SGK3; human; phosphorylation; cancer; diabetes; ischaemia; therapy.
KW
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 77 /note= "O-phosphorylated"
FT Modified-site 79 /note= "O-phosphorylated"
FT
XX
PN WO200035946-A1.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-GB004232.
XX
PR 14-DEC-1998; 98US-0112217P.
PR 19-AUG-1999; 99GB-00019676.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Cohen P, Kobayashi T, Deak M;
XX
DR WPI; 2000-442364/38.
XX
DR N-PSDB; AAA27858.
XX
PT Modulation of serum and glucocorticoid-induced protein kinase (SGK) by phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1) or dephosphorylation, useful for treatment of cancer, diabetes and ischemic diseases.
XX
PS Disclosure; Page 7; 127pp; English.
XX
CC The present sequence is that of human serum and glucocorticoid-induced protein kinase (SGK) isoform 3. SGK (see AAY95279) was initially identified as a glucocorticoid and osmotic stress-responsive gene. SGK3

CC is activated by phosphorylation in a similar manner to SGK. The invention
CC provides methods of activating SGK activity by phosphorylation using 3-
CC phosphoinositide-dependent protein kinase-1 (PDK1), and of reducing the
CC activity of SGK by dephosphorylation. The invention also provides a
CC method of identifying a compound that modulates the activity of SGK. Such
CC compounds are useful for treating patients requiring modulation of SGK,
CC such as patients with cancer, diabetes or ischaemic disease
XX Sequence 429 AA;

Query Match 100.0%; Score 2269; DB 3; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.4e-214;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFQMDSPKHQSD 60
DB 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFQMDSPKHQSD 60
QY 61 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLKGKF 120
DB 61 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLKGKF 120
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
DB 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
QY 181 LFFHLQRRSPFPHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240
DB 181 LFFHLQRRSPFPHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240
QY 241 CKEGIAISDTTTFCTGTPPEVLAPEVIRKOPYDNTVDWCLGAVLYEMLYGLPFPYCRDVA 300
DB 241 CKEGIAISDTTTFCTGTPPEVLAPEVIRKOPYDNTVDWCLGAVLYEMLYGLPFPYCRDVA 300
QY 301 EMYDNILHKPLSLRPGVSLTAWISLELLEKQKQNLGAKEDPLEIQNHPPFFESLSWADL 360
DB 301 EMYDNILHKPLSLRPGVSLTAWISLELLEKQKQNLGAKEDPLEIQNHPPFFESLSWADL 360
QY 361 VQKKIPPPNPNVAGPDDIRNFDTAFTTEETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 420
DB 361 VQKKIPPPNPNVAGPDDIRNFDTAFTTEETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 420
QY 421 APPSEDLFL 429
DB 421 APPSEDLFL 429

RESULT 2
ADN38798
ID ADN38798 standard; protein; 429 AA.

XX AC ADN38798;
XX DT 17-JUN-2004 (first entry)
XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:116.
XX KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN WO2003042661-A2.
XX PD 22-MAY-2003.
XX PF 13-NOV-2002; 2002WO-US036810.
XX

PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-035250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-036809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-039775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX PA
XX PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI: 2003-468649/44.
XX N-PSDB; ADN38797.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO 116; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 429 AA;

Query Match 100.0%; Score 2269; DB 7; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.4e-214;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFQMDSPKHQSD 60
DB 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFQMDSPKHQSD 60
QY 61 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLKGKF 120
DB 61 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDFLKVIGKSGFKVLLAKRKLKGKF 120
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
DB 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
QY 181 LFFHLQRRSPFPHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240
DB 181 LFFHLQRRSPFPHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240

QY 241 CKEGIAISDTTTCGTEPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
 DB 241 CKEGIAISDTTTCGTEPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
 QY 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKORQNLGAKEDFLEIQNHPPFFESLSWADL 360
 DB 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKORQNLGAKEDFLEIQNHPPFFESLSWADL 360
 QY 361 VQKKIPPPFNPVAGPDDIRNFDTAFTETVPYSCVSSDYSIIVNASVLEADDAFVGFSY 420
 DB 361 VQKKIPPPFNPVAGPDDIRNFDTAFTETVPYSCVSSDYSIIVNASVLEADDAFVGFSY 420
 QY 421 APPSEDLFL 429
 DB 421 APPSEDLFL 429
 RESULT 3
 ADY17700
 ID ADY17700 standard; protein; 429 AA.
 AC ADY17700;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE PRO polypeptide SEQ ID NO 3506.
 XX
 KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotrophic;
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FN W02005016962-A2.
 XX
 PD 24-FEB-2005.
 XX
 PF 11-AUG-2004; 2004WO-US026249.
 XX
 PR 11-AUG-2003; 2003US-0493546P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
 XX
 DR WPI; 2005-182330/19.
 XX
 PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
 XX
 PS Claim 8; SEQ ID NO 3506; 158pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
 CC composition, and method are useful for diagnosing and treating an immune
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
 CC arthritis. The present sequence represents a PRO polypeptide.
 XX
 SQ Sequence 429 AA;
 Query Match 100.0%; Score 2269; DB 9; Length 429;
 Best Local Similarity 100.0%; Pred. No. 1.4e-214;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALKIPAKRIFGDNFDPDFIKORRAGNEFIQNLVRYPELYNHPDVRAFQMDSPKQSD 60
 DB 1 MALKIPAKRIFGDNFDPDFIKORRAGNEFIQNLVRYPELYNHPDVRAFQMDSPKQSD 60
 QY 61 PSEDEDRSSQKLHSTSONINLPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGK 120

DB 61 PSEDEDRSSQKLHSTSONINLPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGK 120
 QY 121 YAVKVLQKKIIVLNRKQKHIMAEARNVLLKNVKEPFLVGLHYSFOTTEKLYFVLDFVNGGE 180
 DB 121 YAVKVLQKKIIVLNRKQKHIMAEARNVLLKNVKEPFLVGLHYSFOTTEKLYFVLDFVNGGE 180
 QY 181 LFFHLQERSFPPEHRAFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTFDGL 240
 DB 181 LFFHLQERSFPPEHRAFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTFDGL 240
 QY 241 CKEGIAISDTTTCGTEPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
 DB 241 CKEGIAISDTTTCGTEPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
 QY 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKORQNLGAKEDFLEIQNHPPFFESLSWADL 360
 DB 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKORQNLGAKEDFLEIQNHPPFFESLSWADL 360
 QY 361 VQKKIPPPFNPVAGPDDIRNFDTAFTETVPYSCVSSDYSIIVNASVLEADDAFVGFSY 420
 DB 361 VQKKIPPPFNPVAGPDDIRNFDTAFTETVPYSCVSSDYSIIVNASVLEADDAFVGFSY 420
 QY 421 APPSEDLFL 429
 DB 421 APPSEDLFL 429
 RESULT 4
 AAM40620
 ID AAM40620 standard; protein; 496 AA.
 AC AAM40620;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 5551.
 XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN W0200153312-A1.
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-0052317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AA159776.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.

XX Example 2; SEQ ID NO 5551; 10078pp; English.
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA38642-AA42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 496 AA;

Query Match 100.0%; Score 2269; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-214;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALKIPAKRIFGDNEDPDRFKORRAGLNEFIQNLVRPELYNHPDVRAFLQMDSPKHQSD 60
Db 68 MALKIPAKRIFGDNEDPDRFKORRAGLNEFIQNLVRPELYNHPDVRAFLQMDSPKHQSD 127
QY 61 PSEDEDESSQKLHSTSQINILGSPGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 120
Db 128 PSEDEDESSQKLHSTSQINILGSPGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 187
QY 121 YAVKVLQKTVLNRKQKHIMARNVLLKNVHPFLVGLHYSPQTTEKLYFVLDFVNGGE 180
Db 188 YAVKVLQKTVLNRKQKHIMARNVLLKNVHPFLVGLHYSPQTTEKLYFVLDFVNGGE 247
QY 181 LFPHLORESFPHRARFYAAETASALGYLHSTKIIVYRDLKPENILLDSVGHVVLDFGL 240
Db 248 LFPHLORESFPHRARFYAAETASALGYLHSTKIIVYRDLKPENILLDSVGHVVLDFGL 307
QY 241 CKEGIAISDTTTFCTGPEYLAPEVIRKQPDYNTVDWMCIGAVLYEMLYGLPFYCRDVA 300
Db 308 CKEGIAISDTTTFCTGPEYLAPEVIRKQPDYNTVDWMCIGAVLYEMLYGLPFYCRDVA 367
QY 301 EMYDNLHKPLSLRPGVSLTAWSIILELLEKQRNRLGAKEDFLEIQNHPPFFESLSWADL 360
Db 368 EMYDNLHKPLSLRPGVSLTAWSIILELLEKQRNRLGAKEDFLEIQNHPPFFESLSWADL 427
QY 361 VOKKIPPPNPVAGPDDIRNFDATAETETVPYSCVSDYSIVNASVLEADDAFVGFSY 420
Db 428 VOKKIPPPNPVAGPDDIRNFDATAETETVPYSCVSDYSIVNASVLEADDAFVGFSY 487
QY 421 APPSEDLFL 429
Db 488 APPSEDLFL 496

RESULT 5
AAU87228
ID AAU87228 standard; protein; 496 AA.
XX
AC AAU87228;
XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #138.
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;

KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001332.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0228279P.
PR 22-AUG-2000; 2000US-0228681P.
PR 22-AUG-2000; 2000US-0228688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.


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PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
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PR 08-DEC-2000; 2000US-0251989P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-581633/65.
XX N-PSDB; ABK43538.
XX
XX New isolated nucleic acid encoding a protein for diagnosing, preventing,
XX treating or ameliorating medical conditions and used as food additives or
XX preservatives.
XX
XX Claim 9; SEQ ID NO 746; 837pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX novel central nervous system protein. (I) and polypeptides (III) encoded
XX by (I), are used to treat a medical conditions and in diagnosis of a
XX pathological condition. Disorders which are diagnosed or treated include
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
XX e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
XX angiogenesis, nervous system disorders e.g. Alzheimer's disease and
XX amyotrophic lateral sclerosis, infections caused by bacteria, viruses
XX e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
XX e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
XX adenocarcinomas and irritable bowel syndrome, reproductive system
XX disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
XX and pituitary dwarfism, cancers and disorders at the cellular level e.g.
XX leukaemia, disorders involving neovascularisation e.g. malignancies,
XX respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
XX acute kidney failure and blood related disorders e.g. myocardial
XX infarction. The polypeptides can also be used to aid wound healing and
XX epithelial cell proliferation, to prevent skin aging due to sunburn, to
XX maintain organs before transplantation, for supporting cell culture of
XX primary tissues, to regenerate tissues and in chemotaxis. The
XX polypeptides can also be used as a food additive or preservative to
XX increase or decrease storage capabilities, fat content, lipid, protein,
```

Qy 421 APPSEDLFL 429
Db 488 APPSEDLFL 496

RESULT 6
AAU87382
ID AAU87382 standard; protein; 496 AA.
XX AAU87382;
XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #292.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
XX 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US6001332.
XX
31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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 PR 03-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI
 XX WPI; 2001-581633/65.
 DR N-PSDB; ABK43712.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing, preventing,
 PT treating or ameliorating medical conditions and used as food additives or
 PT preservatives.
 XX
 XX Claim 9; SEQ ID NO 900; 837pp; English.
 PS
 XX The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (II) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC
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 Best Local Similarity 100.0%; Pred. No. 1.7e-214;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB
 68 MALKIPAKRIFGNFDDFKQRRAGLNEFIQNLVPELYNHPDVRAFLQMDSPKHQSD 127
 QY 61 PSEDEDESSQKLHSTSQNLINLPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 120
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Db 128 PSEDEDESSQKLHSTSQNLINLPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 187
 QY 121 YAVKVLQKKIVLNRKQKHIMAEARNVLLKNVKHPFLVGLHYSTQTTTEKLYFVLDPVNGGE 180
 Db 188 YAVKVLQKKIVLNRKQKHIMAEARNVLLKNVKHPFLVGLHYSTQTTTEKLYFVLDPVNGGE 247
 QY 181 LFFHLQERSFPFHRARFYAAEIASALGYLHSLKIVYRDLKPENILLDSVGHVVLTDGFL 240
 Db 248 LFFHLQERSFPFHRARFYAAEIASALGYLHSLKIVYRDLKPENILLDSVGHVVLTDGFL 307
 QY 241 CKEGIAISDTTTFCTGTPPEYLAVEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
 Db 308 CKEGIAISDTTTFCTGTPPEYLAVEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 367
 QY 301 EMDYDNLHKLPLSLRPGVSLTAWSLBELLEKQNRILGAKEDFLEIQNHFFFSLSWADL 360
 Db 368 EMDYDNLHKLPLSLRPGVSLTAWSLBELLEKQNRILGAKEDFLEIQNHFFFSLSWADL 427
 QY 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 420
 Db 428 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 487
 QY 421 APPSEDLFL 429
 Db 488 APPSEDLFL 496
 RESULT 7
 ADIS4543
 ID ADIS4543 standard; protein; 496 AA.
 XX
 AC ADIS4543;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Novel human protein seq id 746.
 XX
 KW neuroprotective; nootropic; antiparkinsonian; anticonvulsant;
 KW antidiabetic; antirheumatic; antiarthritic; dermatological;
 KW antiinflammatory; immunosuppressive; antithyroid; antianemic; vasotropic;
 KW anti-HIV; hepatotropic; virucide; antibacterial; fungicide;
 KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;
 KW cardiovascular; antiarteriosclerotic; antiarrhythmic; cardiac;
 KW nephrotropic; litholytic; cytostatic; gene therapy; neural disorder;
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
 KW amyotrophic lateral sclerosis; multiple sclerosis;
 KW immune system disorder; diabetes; rheumatoid arthritis;
 KW systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;
 KW inflammatory disorder; ischaemia-reperfusion injury;
 KW inflammatory bowel disease; Crohn's disease; infectious disease;
 KW HIV infection; hepatitis infection; bacterial infection;
 KW fungal infection; parasitic infection; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
 KW cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;
 KW renal disorder; acute glomerulonephritis; pyelonephritis;
 KW renal lithiasis; proliferative disorder; cancerous diseases; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004018969-A1.
 XX
 XX 29-JAN-2004.
 XX
 XX 17-JAN-2001; 2001US-00764875.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR

CC sequence at least 90% identical to: a polypeptide fragment, domain,
CC epitope, or full-length protein of any one of 607 amino acid sequences
CC (i) described in the specification; a polypeptide fragment of (i), or the
CC encoded sequence contained in (ii), having biological activity; or a
CC variant, allelic variant, or a species homologue of (i). The polypeptides
CC and nucleic acid molecules are useful for detecting, preventing,
CC diagnosing, prognosticating, treating or ameliorating medical conditions
CC such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease,
CC Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis,
CC immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic

Query Match 100.0%; Score 2269; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. NO. 1.7e-214;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60
Db 68 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 127
Qy 61 PSEDEDRSSQKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKGF 120
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Qy 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTKLYFVLDLVNGGE 180
Db 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTKLYFVLDLVNGGE 247
Qy 181 LFFHLQRFSPFPHRAFYAAETASALGYLHSTKIIVYRDLKPNILLDSVGHVLTDFGL 240
Db 248 LFFHLQRFSPFPHRAFYAAETASALGYLHSTKIIVYRDLKPNILLDSVGHVLTDFGL 307
Qy 241 CKEGIAISDTTTFCTGPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
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Db 368 EMTDNLHLKPLSRPGVSLTAWSLLELLKPKQNLGAKEDFLEIQNHPPFESLSWADL 427
Qy 361 VQKKIPPPNPVAGPDIDRNFDTAFTETVTPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db 428 VQKKIPPPNPVAGPDIDRNFDTAFTETVTPYSCVSSDYSIVNASVLEADDAFVGFSY 487
Qy 421 APPSEDLFL 429
Db 488 APPSEDLFL 496

RESULT 8
ADIS4697
ID ADIS4697 standard; protein; 496 AA.

AC ADIS4697;

XX 22-APR-2004 (first entry)

DE Novel human protein seq id 900.

XX neuroprotective; neurotropic; antiparkinsonian; anticonvulsant;
KW antidiabetic; antirheumatic; antiarthritic; dermatological;
KW antiinflammatory; immunosuppressive; anticholeric; antianemic; vasotrophic;
KW anti-HIV; hepatotropic; virucide; antibacterial; fungicide;
KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;
KW cardiovascular; antiarteriosclerotic; antiarrhythmic; cardiac;
KW nephrotropic; litholytic; cytosolic; gene therapy; neural disorder;
KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
KW amyotrophic lateral sclerosis; multiple sclerosis;
KW immune system disorder; diabetes; rheumatoid arthritis;
KW systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;
KW inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; infectious disease;
KW HIV infection; hepatitis infection; bacterial infection;
KW fungal infection; parasitic infection; muscular disorder;

KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;
KW renal disorder; acute glomerulonephritis; pyelonephritis;
KW renal lithiasis; proliferative disorder; cancerous diseases; human.
XX Homo sapiens.
XX US2004018969-A1.
PD 29-JAN-2004.

XX 17-JAN-2001; 2001US-00764875.
PF 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
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PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
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PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.

PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2004-122079/12.
DR N-PSDB; ADI54099.
XX
PT New polypeptides and nucleic acid molecules, useful for detecting, medical
PT preventing, diagnosing, prognosticating, treating or ameliorating infectious
PT conditions e.g. neural disorders, reproductive disorders or infectious
PT diseases.
XX
XX Claim 11; SEQ ID NO 900; 413pp; English.
XX
CC The invention describes an isolated polypeptide comprising an amino acid
CC sequence at least 90% identical to: a polypeptide fragment, domain,
CC epitope, or full-length protein of any one of 607 amino acid sequences
CC (I) described in the specification; a polypeptide fragment of (I), or the
CC encoded sequence contained in (II), having biological activity; or a
CC variant, allelic variant, or a species homologue of (I). The polypeptides
CC and nucleic acid molecules are useful for detecting, preventing,
CC diagnosing, prognosticating, treating or ameliorating medical conditions
CC such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease,
CC Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis,
CC immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic

Query Match 100.0%; Score 2269; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-214;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
DB 68 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127
QY 61 PSEDEDESSQKLHSTSQINILGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKF 120
DB 128 PSEDEDESSQKLHSTSQINILGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDGKF 187
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 247
QY 181 LFFHLQRESPFPHRARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL 240
DB 248 LFFHLQRESPFPHRARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVLTDFGL 307
QY 241 CKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTDWMCLGAVLYEMLYGLPPFYCRDVA 300
DB 308 CKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTDWMCLGAVLYEMLYGLPPFYCRDVA 367
QY 301 EMYDNLHKPLSLRPGCVSLTAWSIIEELLEKORQNLGAKEDFLEIQNHPPFESLSWADL 360
DB 368 EMYDNLHKPLSLRPGCVSLTAWSIIEELLEKORQNLGAKEDFLEIQNHPPFESLSWADL 427
QY 361 VOKKIPPPNPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
DB 428 VOKKIPPPNPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487
QY 421 APPSEDLFL 429
DB 488 APPSEDLFL 496
RESULT 9
ADQ15046
ID ADQ15046 standard; protein; 496 AA.
XX

AC ADQ15046;
DT 07-OCT-2004 (first entry)
DE Human cancer related polypeptide, 2188.
KW Cancer; angiogenic disorder; cytostatic; antiangiogenic; gene therapy;
KW human.
OS Homo sapiens.
XX WO2004058153-A2.
XX 15-JUL-2004.
XX 16-DEC-2003; 2003WO-US040226.
XX 20-DEC-2002; 2002US-0435108P.
XX 23-DEC-2002; 2002US-0436443P.
XX 07-JAN-2003; 2003US-0438498P.
XX 31-JAN-2003; 2003US-0444370P.
XX 06-FEB-2003; 2003US-0446031P.
XX 11-MAR-2003; 2003US-0453635P.
XX 25-MAR-2003; 2003US-0457199P.
XX 10-APR-2003; 2003US-0462458P.
XX 30-APR-2003; 2003US-0466732P.
XX 08-MAY-2003; 2003US-0469184P.
XX 19-MAY-2003; 2003US-0471663P.
XX 03-JUN-2003; 2003US-0475472P.
XX 12-JUN-2003; 2003US-0478150P.
XX 23-JUN-2003; 2003US-0480631P.
XX 15-JUL-2003; 2003US-0487369P.
XX 29-JUL-2003; 2003US-0490866P.
XX 02-SEP-2003; 2003US-0499614P.
XX 09-OCT-2003; 2003US-0510081P.
XX 06-NOV-2003; 2003US-0517742P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Lightcap ES, Ecsedy JA, Hunter JJ, Macbeth KJ, Nestor MT;
XX WPI; 2004-525772/50.
XX N-PSDB; ADQ15045.
XX Identifying a compound capable of treating cancer or an angiogenic
PT disorder by combining a compound to be tested with e.g., 15986, 2179 or
PT 13249 polypeptide and detecting binding of the test compound to the
PT polypeptide.
XX Claim 1; SEQ ID NO 4; 576pp; English.
XX The invention relates to a novel method for identifying a compound
CC capable of treating cancer or an angiogenic disorder. The method
CC comprises: combining a compound to be tested with a cancer related
CC polypeptide; and detecting binding of the test compound to the
CC polypeptide. The invention further comprises: identifying a subject
CC having or at risk for developing cancer; and treating a subject having a
CC cancer or a cancer characterised by aberrant 15986, 2188, 20743, 9148,
CC 9151, 9791, 44252, 14184, 42461, 8204, 7970, 25552, 21657, 26492, 2411,
CC 15088, 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694, 15701,
CC 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201, 6985, 9883, 12238,
CC 18057, 21617, 39228, 49928, 54476, 62113, 64316, 12264, 32362, 58198,
CC 2887, 3205, 8557, 9600, 9693, 44867, 53058, 55556, 57658, 2208, 10252,
CC 10302, 14218, 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827,
CC 21708, 3801, 64698, 2179 or 13249 cancer related polypeptide activity or
CC nucleic acid expression. The method and compounds have cytostatic and
CC antiangiogenic activities. The cancer related genes may be used in gene
CC therapy to treat disorders. The method is useful in identifying a
CC compound capable of treating cancer or an angiogenic disorder. This
CC sequence represents a human cancer related polypeptide used in the method
XX of the invention.
XX Sequence 496 AA;

Query Match 100.0%; Score 2269; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-214; Indels 0; Gaps 0;
Matches 429; Conservative 0; Mismatches 0;
QY 1 MALKIPAKRIFGDNFDDFIKORRAGLNEFIQNLVRYPELYNHDPVRAFLQMDSPKQSD 60
DB 68 MALKIPAKRIFGDNFDDFIKORRAGLNEFIQNLVRYPELYNHDPVRAFLQMDSPKQSD 127
QY 61 PSEDEERSOKLHSTSONINLGPSGNPHAKPTDFDLKVIKSGSPKVLAKRKLQK 120
DB 128 PSEDEERSOKLHSTSONINLGPSGNPHAKPTDFDLKVIKSGSPKVLAKRKLQK 187
QY 121 YAVKVLQKKIVLNKKEQHIMARNVLLKNVHPFLVGLHVSFOTTEKLYFVLDFVNGGE 180
DB 188 YAVKVLQKKIVLNKKEQHIMARNVLLKNVHPFLVGLHVSFOTTEKLYFVLDFVNGGE 247
QY 181 LFFHLQERSFPPEHRRARFYAAETASALGYLHSLIKIVYRDLKPENILLDSYGHVVLTFDGL 240
DB 248 LFFHLQERSFPPEHRRARFYAAETASALGYLHSLIKIVYRDLKPENILLDSYGHVVLTFDGL 307
QY 241 CKEGIALSDTTTTFCGTPEYLAVEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFCRDVA 300
DB 308 CKEGIALSDTTTTFCGTPEYLAVEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFCRDVA 367
QY 301 EMYDNLHKLPLSLRPGVSLTAWLSILBELLEKQNRILGAKEDFLEIQNHHPFESLSWADL 360
DB 368 EMYDNLHKLPLSLRPGVSLTAWLSILBELLEKQNRILGAKEDFLEIQNHHPFESLSWADL 427
QY 361 VQKKIPPPNPVAGPDDIRNFDTAFTETVPYSCVSSDYISVNASVLEADDAFVGFSY 420
DB 428 VQKKIPPPNPVAGPDDIRNFDTAFTETVPYSCVSSDYISVNASVLEADDAFVGFSY 487
QY 421 APPESEDLFL 429
DB 488 APPESEDLFL 496
RESULT 10
AAW87772
ID AAW87772 standard; protein; 496 AA.
XX AC AAW87772;
XX DT 17-MAR-1999 (first entry)
XX DE Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.
XX KW Serum glucocorticoid-regulated kinase; H-SGK2; human; gene therapy;
KW serine/threonine protein kinase; inflammation; rheumatoid arthritis;
KW septicemia; autoimmune disease; inflammatory bowel disease; psoriasis;
KW transplant rejection; infection; stroke; ischaemia; renal disorder;
KW restenosis; brain injury; acquired immune deficiency syndrome; AIDS;
KW metabolic; bone; osteoporosis; lymphoproliferation; atherosclerosis;
KW Alzheimer's disease; cancer.
XX OS Homo sapiens.
XX PF EP889127-A1.
XX PD 07-JAN-1999.
XX PF 18-JUN-1998; 98EP-00304830.
XX PR 01-JUL-1997; 97US-0051446P.
XX PR 23-DEC-1997; 97US-00997212.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PI Kumar S, Zou C;
XX WPI; 1999-062658/06.
XX N-PSDB; AAV99653.

XX New nucleic acid encoding human H-SGK2 poly-peptide(s) - useful for
PT diagnosis, treatment and prevention of e.g. arthritis, infections,
PT cancer, Alzheimer's disease.
XX
PS Claim 11; Page 8; 27pp; English.
XX
XX This represents a human serum glucocorticoid-regulated kinase (H-SGK2)
CC polypeptide, a novel member of the serine/threonine protein kinase
CC family. A host cell transfected or transformed with an expression system
CC comprising the H-SGK2 nucleic acid can be used for the recombinant
CC production of the protein. The H-SGK2 polypeptide is useful for treating
CC a subject who require enhanced/reduced activity or expression/inhibition
CC of the polypeptide. Recombinant H-SGK2 is used to raise antibodies; in
CC vaccines; in drug screens; and to identify soluble or membrane-bound
CC receptors. The H-SGK2 polypeptides are useful for treating inflammation
CC (rheumatoid arthritis); septicemia; autoimmune disease (inflammatory
CC bowel disease or psoriasis); transplant rejection; infection; stroke;
CC leukaemia; renal disorders; restenosis; brain injury; acquired immune
CC deficiency syndrome; metabolic and other bone diseases (osteoporosis);
CC cancer (e.g. lymphoproliferation); atherosclerosis and Alzheimer's
XX disease. The H-SGK2 nucleic acids can be used in gene therapy
XX
SQ Sequence 496 AA;

Query Match 99.7%; Score 2263; DB 2; Length 496;
Best Local Similarity 99.8%; Pred. No. 6.7e-214;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
DB 68 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127
QY 61 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 120
DB 128 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 187
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVLDVFNGGE 180
DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVLDVFNGGE 247
QY 181 LFFHLQERSFPFHRARFYAAETASALGYLHSTKIYVRDLKPNILLDSVGHVLLTDFGL 240
DB 248 LFFHLQERSFPFHRARFYAAETASALGYLHSTKIYVRDLKPNILLDSVGHVLLTDFGL 307
QY 241 CKEGIAISDTTTFCTGTEPEYLAPEVIRKQPYDNTVDWCIGAVLYEMLYGLPPFYCRDVA 300
DB 308 CKEGIAISDTTTFCTGTEPEYLAPEVIRKQPYDNTVDWCIGAVLYEMLYGLPPFYCRDVA 367
QY 301 EMYDNLHKPLSLRPGVSLTAWSLBELLEKQRNLGAKEDPLEIQNHPPFFESLSWADL 360
DB 368 EMYDNLHKPLSLRPGVSLTAWSLBELLEKQRNLGAKEDPLEIQNHPPFFESLSWADL 427
QY 361 VQKKIPPPNPNVAGDDIRNFDFTAFTEETVPYSCVSDYSIVNASVLEADDAFVGFSY 420
DB 428 VQKKIPPPNPNVAGDDIRNFDFTAFTEETVPYSCVSDYSIVNASVLEADDAFVGFSY 487
QY 421 APPSEDLFL 429
DB 488 APPSEDLFL 496

RESULT 11
AAM38834
ID AAM38834 standard; protein; 496 AA.
XX
AC AAM38834;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 1979.
XX
KW Human; neutrotropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
XX N-PSDB; AAI57990.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 3; SEQ ID NO 1979; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neutrotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression.
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
SQ Sequence 496 AA;

Query Match 99.3%; Score 2254; DB 4; Length 496;
Best Local Similarity 99.5%; Pred. No. 5.1e-213;
Matches 427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
DB 68 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127
QY 61 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 120
DB 128 PSEDEDESSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLDDGKF 187
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVLDVFNGGE 180
DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVLDVFNGGE 247
QY 181 LFFHLQERSFPFHRARFYAAETASALGYLHSTKIYVRDLKPNILLDSVGHVLLTDFGL 240

Db 248 LFFHLQERSFPEHRAFYAAETASALGYLHLSIKIVYRDLKPNILDSVGHVLTDFGL 307
Qy 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
Db 308 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVA 367
Qy 301 EMDYDNLHKLPLSLRPGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFESLSWADL 360
Db 368 EMDYDNLHKLPLSLRPGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFESLSWADL 427
Qy 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSCVSSDYISVNASVLEADDAFVGFSY 420
Db 428 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSCVSSDYISVNASVLEADDAFVGFSY 487
Qy 421 APPSEDLFL 429
Db 488 APPSEDLFL 496
RESULT 12
AAB24114
ID AAB24114 standard; protein; 429 AA.
AC AAB24114;
XX 29-JAN-2001 (first entry)
XX Human serine threonine kinase STK3 protein sequence SEQ ID NO:4.
DE Human; STK3; serine threonine kinase; HSGK; RSGK;
KW serum and glucocorticoid regulated kinase.
XX Homo sapiens.
XX CN1259573-A.
XX 12-JUL-2000.
XX 29-OCT-1998; 98CN-00123822.
XX 29-OCT-1998; 98CN-00123822.
XX (UYFU-) UNIV FUDAN.
XX Yu L, Fu Q, Zhao Y;
XX WPI; 2000-587991/56.
DR N-PSDB; AAA99248.
XX New human serine threonine protein kinase, its code sequence,
PT preparation, and use.
XX Claim 4; Page 19; 29pp; Chinese.
XX The present invention describes human serine threonine kinase STK3, which
CC is a new member of the serine/threonine protein kinase family. Human STK3
CC shares homology with human serum and glucocorticoid regulated kinase
CC (HSGK) and rat SGK (RSGK). The present sequence represents the human STK3
CC protein from the present invention
XX
SQ Sequence 429 AA;
Query Match 99.0%; Score 2246; DB 3; Length 429;
Best Local Similarity 99.1%; Pred. No. 2.6e-212;
Matches 425; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MALKIPAKRIFGNFDFIKQRRAGINEFIQNLVRYPELYNHPDVRFLQWDSPKHQSD 60
Db 1 MALKIPAKRIFGNFDFIKQRRAGINEFIQNLVRYPELYNHPDVRFLQWDSPKHQSG 60
Qy 61 PSEDEDESSQKLHSTSQNINLGPSONPHAKPTDFDLKVIKGSFGKVLAKRKLKDGK 120

Db 61 PSEDEDESSQKLHSTSQNINLGPSONPHAKPTDFDLKVIKGSFGKVLAKRKLKDGK 120
Qy 121 YAVKVLQKKIVLNRKEQKHIMAEARNVLLKNVXHPFLVGLHYHSQTTEKLYFVLDFVNGGE 180
Db 121 YAVKVLQKKIVLNRKEQKHIMAEARNVLLKNVXHPFLVGLHYHSQTTEKLYFVLDFVNGGE 180
Qy 181 LFFHLQERSFPEHRAFYAAETASALGYLHLSIKIVYRDLKPNILDSVGHVLTDFGL 240
Db 181 LFFHLQERSFPEHRAFYAAETASALGYLHLSIKIVYRDLKPNILDSVGHVLTDFGL 240
Qy 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
Db 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
Qy 301 EMDYDNLHKLPLSLRPGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFESLSWADL 360
Db 301 EMDYDNLHKLPLSLRPGVSLRANSLLELLEKQDNRLGAKEDFLEIQNHPPFESLSWADL 360
Qy 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSCVSSDYISVNASVLEADDAFVGFSY 420
Db 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSCVSSDYISVNASVLEADDAFVGFSY 420
Qy 421 APPSEDLFL 429
Db 421 APPSEDLFL 429
RESULT 13
ADRL4041
ID ADRL4041 standard; protein; 496 AA.
XX AC ADRL4041;
XX DT 21-OCT-2004 (first entry)
XX Human NF-kappaB pathway-associated protein SeqID42.
DE NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnery; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IGM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; human.
XX Homo sapiens.
XX WO2004065577-A2.
XX 05-AUG-2004.
XX 13-JAN-2004; 2004WO-US0000798.
XX 14-JAN-2003; 2003US-0440068P.
PR 12-MAY-2003; 2003US-0469757P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Nadler SG, Neubauer MG, Feder JN, Carman J;
PI WPI; 2004-562168/54.
XX DR N-PSDB; ADRL4040.
XX

PT New isolated polynucleotides and polypeptides associated with NF-kappaB
PT pathway, useful for diagnosing, treating, or preventing disorders or
PT diseases associated with NF-kappaB pathway.

XX
PS Claim 6; SEQ ID NO 42; 237pp; English.

This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic, gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnery activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant signal transduction, proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human protein which is subject to the novel association with the NF-kappaB pathway of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.

Sequence 496 AA;

Query Match	99.0%;	Score 2246;	DB 8;	Length 496;
Best Local Similarity	99.1%;	Pred. No. 3.2e-212;		
Matches 425;	Conservative	1;	Mismatches 3;	Indels 0;
Gaps	0;			

1	Qy	1	MAL	KI	PAKR	I	FGDN	FD	PD	F	I	KOR	PAG	L	NE	F	T	Q	N	L	V	R	P	E	L	Y	N	H	D	V	R	A	F	L	O	M	D	S	P	K	H	S	D	60																
68	Db	68	MAU	KI	PAKR	I	FGDN	FD	PD	F	I	KOR	PAG	L	NE	F	T	Q	N	L	V	R	P	E	L	Y	N	H	D	V	R	A	F	L	O	M	D	S	P	K	H	S	D	127																
61	Qy	61	P	S	E	D	E	D	R	S	S	O	K	L	H	S	T	S	Q	N	I	N	L	G	S	G	N	H	P	A	K	T	D	F	L	K	V	I	G	K	S	F	G	V	L	A	K	R	L	D	K	G	F	120						
128	Db	128	P	S	E	D	E	D	R	S	S	O	K	L	H	S	T	S	Q	N	I	N	L	G	S	G	N	H	P	A	K	T	D	F	L	K	V	I	G	K	S	F	G	V	L	A	K	R	L	D	K	G	V	187						
121	Qy	121	Y	A	V	K	L	O	K	K	I	V	L	N	R	K	E	O	K	H	I	M	A	E	R	N	V	L	L	K	N	V	K	H	P	F	L	V	G	L	H	Y	S	P	O	T	E	K	L	Y	F	V	L	D	P	V	N	G	E	180
188	Db	188	Y	A	V	K	L	O	K	K	I	V	L	N	R	K	E	O	K	H	I	M	A	E	R	N	V	L	L	K	N	V	K	H	P	F	L	V	G	L	H	Y	S	P	O	T	E	K	L	Y	F	V	L	D	P	V	N	G	E	247
181	Qy	181	L	F	H	L	O	R	S	F	P	E	H	R	A	P	Y	A	E	I	A	S	A	L	G	Y	L	H	S	I	K	I	V	R	D	L	K	P	E	N	I	L	D	S	V	G	H	V	L	T	D	F	G	L	240					
248	Db	248	L	F	H	L	O	R	S	F	P	E	H	R	A	P	Y	A	E	I	A	S	A	L	G	Y	L	H	S	I	K	I	V	R	D	L	K	P	E	N	I	L	D	S	V	G	H	V	L	T	D	F	G	L	307					
241	Qy	241	C	K	E	G	I	A	S	D	T	T	T	P	C	G	T	P	E	V	L	A	P	E	V	I	R	K	Q	P	D	N	T	V	D	M	W	C	L	G	A	V	Y	E	M	L	Y	G	L	P	P	F	Y	C	R	D	V	A	300	
308	Db	308	C	K	E	G	I	A	S	D	T	T	T	P	C	G	T	P	E	V	L	A	P	E	V	I	R	K	Q	P	D	N	T	V	D	M	W	C	L	G	A	V	Y	E	M	L	Y	G	L	P	P	F	Y	C	R	D	V	A	367	
301	Qy	301	E	M	Y	D	N	I	L	H	K	P	L	S	R	P	G	V	S	L	T	A	W	S	I	E	L	L	E	K	D	R	Q	N	R	L	G	A	K	E	D	F	I	E	I	Q	N	H	P	P	F	E	S	L	S	W	A	D	L	360
368	Db	368	E	M	Y	D	N	I	L	H	K	P	L	S	R	P	G	V	S	L	T	A	W	S	I	E	L	L	E	K	D	R	Q	N	R	L	G	A	K	E	D	F	I	E	I	Q	N	H	P	P	F	E	S	L	S	W	A	D	L	427
361	Qy	361	V	O	K	K	I	P	P	E	N	P	N	V	A	G	P	D	I	R	N	F	D	T	A	F	T	E	E	T	V	P	Y	S	C	V	S	S	D	Y	S	I	V	N	A	S	V	L	E	A	D	D	A	F	V	G	F	S	Y	420
428	Db	428	V	O	K	K	I	P	P	E	N	P	N	V	A	G	P	D	I	R	N	F	D	T	A	F	T	E	E	T	V</																													

RESULT 14
ADY18746

ADY18746
ID ADY18746 standard; protein; 397 AA.

XX
AC

DT 05-MAY-2005 (first entry)

DE PRO polypeptide SEQ ID NO 4552.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Varicic; Gastrointestinal-Gen.; Antipsoriatic; Antiaslathmatic;
KW Antiallergic; diagnosis.

XX
OS Homo sapiens.

XX
PN WO2005016962-A2.

XX
PD 24-FEB-2005

XX
PF 11-AUG-2004; 2004WO-US026249.

XX
PR 11-AUG-2003; 2003US-0493546P.

XX
PA (GETH) GENENTECH INC.

XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX
DR WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus

XX
PS Claim 8; SEQ ID NO 4552; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a PRO polypeptide.

XX
SQ Sequence 397 AA;

Query Match 90.8%; Score 2061; DB 9; Length 397;
Best Local Similarity 92.5%; Pred. No. 4.2e-194;

[illegible]

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2006, 23:21:11 ; Search time 20.2358 Seconds
(without alignments)
1752.724 Million cell updates/sec

Title: US-09-868-131A-4
Perfect score: 2269
Sequence: 1 MALKIPAKRIFGDNFDPDFI.....EADDAFVGFSYAPPSDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1476	65.1	407	2	US-10-067-977-4
2	1476	65.1	445	2	US-10-067-977-2
3	1472	64.9	431	2	US-09-031-295-2
4	1472	64.9	431	2	US-10-000-039-2
5	1468	64.7	431	1	US-08-712-709-5
6	1468	64.7	431	2	US-09-111-444-5
7	1468	64.7	431	2	US-09-541-228-5
8	1458.5	64.3	430	1	US-08-712-709-9
9	1458.5	64.3	430	2	US-09-111-444-9
10	1458.5	64.3	430	2	US-09-541-228-9
11	870	38.3	465	2	US-09-526-043-2
12	866.5	38.2	479	2	US-09-771-161A-246
13	866.5	38.2	479	2	US-09-771-161A-247
14	866.5	38.2	479	2	US-09-771-161A-248
15	860.5	37.9	454	2	US-09-526-043-17
16	844.5	37.2	480	2	US-09-526-043-13
17	844.5	37.2	481	2	US-09-538-092-1054
18	818.5	36.1	480	2	US-09-590-740-6
19	818.5	36.1	726	2	US-09-417-197-71
20	816.5	36.0	480	2	US-09-091-058-2
21	816.5	36.0	480	2	US-09-590-740-2
22	816.5	36.0	480	2	US-09-538-092-1053
23	816.5	36.0	480	2	US-09-526-043-14
24	816.5	36.0	480	2	US-09-771-161A-223
25	816.5	36.0	727	2	US-09-417-197-139
26	803.5	35.4	587	1	US-08-313-274-2
27	803.5	35.4	655	2	US-09-949-016-11676

28	792	34.9	417	2	US-09-590-740-4	Sequence 4, Appli
29	790.5	34.8	737	2	US-09-772-647-4	Sequence 4, Appli
30	790.5	34.8	737	2	US-10-228-931-4	Sequence 4, Appli
31	789	34.8	525	1	US-08-749-902-7	Sequence 7, Appli
32	789	34.8	525	1	US-08-749-902-8	Sequence 8, Appli
33	789	34.8	525	2	US-09-430-564-16	Sequence 16, Appli
34	789	34.8	525	2	US-09-762-258-4	Sequence 157, App
35	788.5	34.8	480	2	US-09-205-658-157	Sequence 996, App
36	787.5	34.7	502	2	US-09-538-092-996	Sequence 2, Appli
37	786	34.6	482	2	US-09-430-564-2	Sequence 3, Appli
38	786	34.6	495	2	US-09-430-564-3	Sequence 2, Appli
39	786	34.6	495	2	US-09-762-258-2	Sequence 2, Appli
40	784	34.6	470	2	US-09-248-796A-18482	Sequence 18482, A
41	779.5	34.4	737	2	US-09-771-161A-195	Sequence 195, App
42	763	33.6	672	2	US-10-092-138A-27	Sequence 27, Appl
43	763	33.6	672	2	US-09-538-092-943	Sequence 943, App
44	763	33.6	672	2	US-08-681-219A-27	Sequence 27, Appl
45	760.5	33.5	546	2	US-09-205-658-155	Sequence 155, App

ALIGNMENTS

RESULT 1

US-10-067-977-4
; Sequence 4, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-067-977-4

Query Match	65.1%	Score 1476;	DB 2;	Length 407;
Best Local Similarity	67.5%	Pred. No. 3.9e-134;		
Matches	280;	Conservative	52;	Mismatches 69;
			Indels	14;
			Gaps	3;
Qy	19	FIKQRAGLNEFTQNLVRYPELYNHPDVRFLQMDSPKH----	QSDPSEDEBSSOKLH	74
Db	3	FMKQRMGLNDFIQKIANNYSACKHPEVQSIKISQBPPELMNANPSPPP-----	53	
Qy	75	STSQNLGPGSNPHAKPTDFPLKVIKIGSGFKVLLAKRKLDKGYAVKVLQKKIVLNR	134	
Db	54	SPSQNLGPGSNPHAKPSDFHFLKVIKIGSGFKVLLARHKAEEVFYAVKVLQKKAILKK	113	
Qy	135	KEQKHIMARNVLLKNVHPGLVGLHVSFTTEKLYFVLDFVNGGELFELHQLERSPEH	194	
Db	114	KBEKHIMSRNVLNKNVHPGLVGLHVSFTQADKLYFVLDFVNGGELFELHQLERSPEH	173	
Qy	195	RARFYAAETASALGYLHSIKIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF	254	
Db	174	RARFYAAETASALGYLHSINIVYRDLPENILDSQGHIVLTDFGLCKENIENSTSTP	233	
Qy	255	CGTPEYLAPEVIRKQPDYNTVDWMLGAVLYEMLYGLPPYCRDVAEMYNILHKPLSLR	314	
Db	234	CGTPEYLAPEVLHKQPDYRTVDWMLGAVLYEMLYGLPPYCRDVAEMYNILHKPLQLK	293	
Qy	315	PGVSLTAMSLLELLEKQRNRLGAKEDFLEIQNHFFESLSWADLVOKKIPPEFNPVA	374	
Db	294	FNITTSARHLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLLINKKITPPFPNPVS	353	
Qy	375	GPDDIRNFOTAFTEETVPYSCVSSDYISVNASVLEADDAFVGFSYAPPSDLFL	429	

COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/000,039
FILING DATE: 04-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/031,295
FILING DATE: 26-FEB-1998
APPLICATION NUMBER: DE 197-08-173.8
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 058315/0123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-000-039-2

Query Match 64.9%; Score 1472; DB 2; Length 431;
Best Local Similarity 67.2%; Pred. No. 1e-133;
Matches 279; Conservative 53; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKQRAGLNEFTQNLVRYPELYNHPDVRAFLQMDSPKH----QSDPSEDEDRSSQKLH 74
DB 27 FMKQRRMGLNDFQKIANNSSYACKHPEVQSILKISQBPPELMNANPSPPP----- 77
QY 75 STSQNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKYAVKVLQKIVLNR 134
DB 78 SPSSQNLGPGSSNPHAKPSDFHLKVIKGSFGKVLAKRKAEEVYAVKVLQKAILKK 137
QY 135 KEQKHIMAEARNVLLKNVHPFLVGLHYSTQTEKLYFVLDFVNGGELFFHLQERSGPEH 194
DB 138 KEKHIMSERVLLKNVHPFLVGLHFSFQTADKLYFVLVDYINGGELFFHLQERCFLPE 197
QY 195 RARFYAAEIASALGYLHSIKIVYRDLKPENILLDSQGHVLTDFGLCKEGIAISDTTTF 254
DB 198 RARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHVLTDFGLCKENIEHNSTTF 257
QY 255 CGTPEYLAPEVIRKQDYNTVDMWCLGAVLYEMLYGLPPPYCRDVAEMVDNILHKPLSLR 314
DB 258 CGTPEYLAPEVLHQPYDRVDMWCLGAVLYEMLYGLPPPYSRNTAEMVDNILKPLQLK 317
QY 315 PGVSLTAWSLLELLEKQRNLGAKEDFLEIQNHPPFESLSWADLVOKKI PPPFPNVA 374
DB 318 PNITNSARHLLGGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVS 377
QY 375 GPDDIRNFDFTAFTEETVPYSCVSSDYISVNAVLDAADFVGFSAAPPSEDLF 429
DB 378 GPNELRHFDPEFTEEPVPSIGKSPDSVLVTASVKEAEAFLGFSYAPPT-DSFL 431

RESULT 5
US-08-712-709-5
; Sequence 5, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 712-709-5
US-08-712-709-5

Query Match 64.7%; Score 1468; DB 1; Length 431;
Best Local Similarity 67.2%; Pred. No. 2.5e-133;
Matches 279; Conservative 52; Mismatches 70; Indels 14; Gaps 3;

QY 19 FIKQRAGLNEFTQNLVRYPELYNHPDVRAFLQMDSPKH----QSDPSEDEDRSSQKLH 74
DB 27 FMKQRRMGLNDFQKIANNSSYACKHPEVQSILKISQBPPELMNANPSPPP----- 77
QY 75 STSQNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKYAVKVLQKIVLNR 134
DB 78 SPSSQNLGPGSSNPHAKPSDFHLKVIKGSFGKVLAKRKAEEVYAVKVLQKAILKK 137
QY 135 KEQKHIMAEARNVLLKNVHPFLVGLHYSTQTEKLYFVLDFVNGGELFFHLQERSGPEH 194
DB 138 KEKHIMSERVLLKNVHPFLVGLHFSFQTADKLYFVLVDYINGGELFFHLQERCFLPE 197
QY 195 RARFYAAEIASALGYLHSIKIVYRDLKPENILLDSQGHVLTDFGLCKEGIAISDTTTF 254
DB 198 RARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHVLTDFGLCKENIEHNSTTF 257
QY 255 CGTPEYLAPEVIRKQDYNTVDMWCLGAVLYEMLYGLPPPYCRDVAEMVDNILHKPLSLR 314
DB 258 CGTPEYLAPEVLHQPYDRVDMWCLGAVLYEMLYGLPPPYSRNTAEMVDNILKPLQLK 317
QY 315 PGVSLTAWSLLELLEKQRNLGAKEDFLEIQNHPPFESLSWADLVOKKI PPPFPNVA 374
DB 318 PNITNSARHLLGGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVS 377
QY 375 GPDDIRNFDFTAFTEETVPYSCVSSDYISVNAVLDAADFVGFSAAPPSEDLF 429
DB 378 GPNELRHFDPEFTEEPVPSIGKSPDSVLVTASVKEAEAFLGFSYAPPT-DSFL 431

RESULT 6
US-09-111-444-5
; Sequence 5, Application US/09111444
; Patent No. 6045792

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Dd	136	: : : : : : : : : : :	
Dd	138	KEEKHTMSERNVLLKNVKHPFLVLGHFSFOQADKLYFVLDYINGEGLFYHLQERCFLPE	197
		: : : : : : : : : :	
Qy	195	RARFYAAETASALGYLHSIKIIVYRDLKENILLDSVGHVLTDFGLCKEGAIASDTTTTF	254
Dd	198	RARFYAAETASALGYLHSINIVYRDLKENILLDSOGHI VLTDFGLCKENIEHGTTSTP	257
		: : : : : : : : : :	
Qy	255	CQTPEYLAPEVIKRPDYNTDVMWCLGAVLYEMLYGLPPFCRDVAEMYNILHKPLSLR	314
Dd	258	CQTPEYLAPEVLHKPYDKTVDWMWCLGAVLYEMLYGLPPFSRNATSMYNILNKPLQLK	317
		: : : : : : : : : :	
Qy	315	PGVSLTAWSILBELLEKQRNRLGAKEDFLETQNHPFSESISWADLYQKKIPPEPNVNA	374
Dd	318	-NITN-ARHLHBGLIQOKRTKRLGAKDDFMEEKSHIFPSFLINWDLLINKKITTPFPNPVS	376
		: : : : : : : : : :	
Qy	375	GPDIDINFDTAFTETVPYSVCVSDSYIVNASVLEADDAPFGVFSYAPPSEDLF	429
Dd	377	GPSDLRHFPDETEEPVSSIGRSPOSILVTASTVKRAEAAPLGFSYAPP-DSFL	430

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RESULT 10
US-09-541-228-9
; Sequence 9, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

NAME: BILLINGS, LUCY J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:

Db	27	FMQRRMGLNDFIQKLANNYSACKHPVQSYLKI SQQPELMANPSPPP-----	77
Qy	75	STSONINLPGSNPHAKPTDFDLKVIGKSGFGVLLAKRKLDCKFYAVKVLQKKI VLNR	134
Db	78	SPSQINLGPSSNPHAKPSDFHUKVIGKSGFGVKLLARHKAESAFYAVKVLQKKA LUK	137
Qy	135	KEQKHMAERNVLLKNVKHPLVGLHYSFQTTEKLYFVLDPVNGGELFFHQLQRERSFP	194
Db	138	KEEKHINSERNVLLKNVKHPLVGLHYSFQTADKLYFVLDPVNGGELFYHLQRERCFL	197
Qy	195	RARFYAAEIASALGYLHSIKIVYRDLKPNILLDVGHVLTDFGLCKEGIAISDTTTF	254
Db	198	RARFYAAEIASALGYLHSILNIVYRDLKPNILLDVGHVLTDFGLCKENIEHNGTST	257
Qy	255	CGTPEYLAPSVIRKQPDYNTVDWMLGAVLYEMLYGLPPFCYRDAEMYDNILHKPLSR	314
Db	258	CGTPEYLAPSVLHKQPDYNTVDWMLGAVLYEMLYGLPPFYSRNTAEMYDNILKPLQK	317
Qy	315	PGVSLTAWSLTEELLEKDRQNLGAKEDFLIEIQNHPPFESLSWADLVQKKIPPPNPVA	374
Db	318	-NITNSARHLEGLLQKDKTRELGAQDDFMEIKSHIFFSLINWDDLINKKITPPNPVS	376
Qy	375	GPDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAFVGFSYAPPSDDLFL	429
Db	377	GPSDLRHFDFETEEPVPSSIGRSPDSILVTASVKEAAEAPLGFSYAPPM-DSFL	430
RESULT 11			
US-09-526-043-2			
; Sequence 2, Application US/09526043			
; Patent No. 6881555			
; GENERAL INFORMATION:			
; APPLICANT: Guo, Kun			
; APPLICANT: Pagnoni, Marco			
; APPLICANT: Clark, Kenneth			
; APPLICANT: Ivashchenko, Yuri			
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF			
; FILE REFERENCE: A3278A-US			
; CURRENT APPLICATION NUMBER: US/09/526,043			
; CURRENT FILING DATE: 2000-03-14			
; EARLIER APPLICATION NUMBER: 60/125,108			
; EARLIER FILING DATE: 1999-03-19			
; NUMBER OF SEQ ID NOS: 17			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 2			
; LENGTH: 465			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-526-043-2			
Query Match 38.3%; Score 870; DB 2; Length 465;			
Best Local Similarity 45.2%; Pred.No.2e-75;			
Matches 182; Conservative 61; Mismatches 130; Indels 30; Gaps 8			
Qy	20	IKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSE-----	68
Db	62	MKTERPXPNTFIIRCLQWTV-----IERFHVDTPEREETWTAIQAVADRLQREER	116
Qy	69	SSQKLHSTSNINLG-----PSGNPHAKPT--DFDFLKVIGKSGFGVKLLAKRKL	121
Db	117	--MNCSPTSQIDNIGEEEMDASTTHHKRKTWMDFDYLLKLGKTFGKVLVREKASGKY	174
Qy	122	AVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPLVGLHYSFQTEKLYFVLDPVNGGEL	181
Db	175	AMKILKEVNTIAKDEVAHTLTESRV-LKNTRHPEFLTSLKYSFQTKDLRCFCFMYVNG	233
Qy	182	FEHLQRERSPPEHRRARFYAAEIASALGYLHSIKIVYRDLKPNILLDVGHVLTDFGL	241
Db	234	FFHLUSRRVSEDKTRYGAEIVSALDYLSHGKIVYRDLKLENMLDKDGHIKITDFGL	293
Qy	242	KEGIAISDTTTFTCGTPPEYLAPSVIRKQPDYNTVDWMLGAVLYEMLYGLPPFCYR	301

;
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 248
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-248

Query Match 38.2%; Score 866.5; DB 2; Length 479;
Best Local Similarity 43.7%; Pred. No. 4.5e-75;
Matches 184; Conservative 65; Mismatches 145; Indels 27; Gaps 7;
QY 20 IKORRAGLNEFTONLVRYPELYNHPDVRAFLQWDSPKHQSDPSE-----DEDER 68
Db 62 MKTERPKPNTFIIRCLQWTTV-----IERTFHVDTPEEREWEATEAQAVADRLQROEER 116
QY 69 SSQKLHSTQNINLG-----PSGNPHAKPT--DPDFLKVIGKSGFGKVLAKRKLQDGEY 121
Db 117 --MNCSPTSQIDNIGSEEMDASTTHHKRTKTMNDFYLLKLGKGTGKVLVREKASGKY 174
QY 122 AVKVLQKKIVLNRKEQKHIMAERNVLLKNVGHFPLVGLHYSFQTTTEKLYFVLDPVNGGEL 181
Db 175 AMKILKKEVIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGEL 233
QY 182 FFHLQERSFPPEHRARFYAAEIASALGYLHSIKIVYRDLKPNILDSVGHVVLTDGFLC 241
Db 234 FFHLRSRVFSEDRTRFYGAIEVSALDYLHSGKIVYRDLKLENMLDKDGHKIKITDFGLC 293
QY 242 KEGIALSDTTTTCGTPPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCDVAE 301
Db 294 KEGITDAATMKTFCGTPPEYLAPVLENDNDYGRAVDWMLGVVYEMMCGRLPFYNQDHEK 353
QY 302 MYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNL-GAKEDFLEIQNHPPFESLSWADL 360
Db 354 LFEILIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRLOGGPDPAKEIMRHSFFSGVNWQDV 413
QY 361 VQKIPPPNPNVAGPDDIRNFTAFTEETVPSYVCVSDYSIVNASVLEADDAFVGFSY 420
Db 414 YDKKLVPFPKPOVTSETDTRYFDEEFTAQTITITTPPEKYDEDMCDMNERRPHFPQFSY 473
QY 421 A 421
Db 474 S 474

RESULT 15
US-09-526-043-17
; Sequence 17, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-526-043-17

Query Match 37.9%; Score 860.5; DB 2; Length 454;
Best Local Similarity 45.5%; Pred. No. 1.6e-74;
Matches 178; Conservative 61; Mismatches 125; Indels 27; Gaps 7;
QY 20 IKORRAGLNEFTONLVRYPELYNHPDVRAFLQWDSPKHQSDPSE-----DEDER 68
Db 62 MKTERPKPNTFIIRCLQWTTV-----IERTFHVDTPEEREWEATEAQAVADRLQROEER 116
QY 69 SSQKLHSTQNINLG-----PSGNPHAKPT--DPDFLKVIGKSGFGKVLAKRKLQDGEY 121
Db 117 --MNCSPTSQIDNIGSEEMDASTTHHKRTKTMNDFYLLKLGKGTGKVLVREKASGKY 174
QY 122 AVKVLQKKIVLNRKEQKHIMAERNVLLKNVGHFPLVGLHYSFQTTTEKLYFVLDPVNGGEL 181
Db 175 AMKILKKEVIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGEL 233
QY 182 FFHLQERSFPPEHRARFYAAEIASALGYLHSIKIVYRDLKPNILDSVGHVVLTDGFLC 241
Db 234 FFHLRSRVFSEDRTRFYGAIEVSALDYLHSGKIVYRDLKLENMLDKDGHKIKITDFGLC 293
QY 242 KEGIALSDTTTTCGTPPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCDVAE 301
Db 294 KEGITDAATMKTFCGTPPEYLAPVLENDNDYGRAVDWMLGVVYEMMCGRLPFYNQDHEK 353
QY 302 MYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNL-GAKEDFLEIQNHPPFESLSWADL 360
Db 354 LFEILIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRLOGGPDPAKEIMRHSFFSGVNWQDV 413
QY 361 VQKIPPPNPNVAGPDDIRNFTAFTEETV 391
Db 414 YDKKLVPFPKPOVTSETDTRYFDEEFTAQTI 444

Search completed: January 27, 2006, 23:33:31
Job time : 21.2358 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:31:20 ; Search time 75.2774 Seconds
(without alignments)
2381.178 Million cell updates/sec

Title: US-09-868-131A-4
Perfect score: 2269
Sequence: 1 MALKIPAKIFGNFDPDFI.....EADDAFVGFSYAPPSDLFL 429

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2269	100.0	429	4	US-10-295-027-116
2	2269	100.0	496	3	US-09-764-875-746
3	2269	100.0	496	3	US-09-764-875-900
4	2269	100.0	496	5	US-10-737-450-4
5	2263	99.7	496	3	US-09-784-249-2
6	2246	99.0	496	4	US-10-755-889-42
7	1501	66.2	526	4	US-10-094-749-1861
8	1476	65.1	407	4	US-10-067-977-4
9	1476	65.1	407	4	US-10-827-272-4
10	1476	65.1	431	3	US-09-381-353-7
11	1476	65.1	431	4	US-10-403-161-2
12	1476	65.1	431	4	US-10-403-161-4
13	1476	65.1	445	4	US-10-067-977-2
14	1476	65.1	445	4	US-10-827-272-2
15	1472	64.9	431	4	US-10-000-039-2
16	1472	64.9	431	4	US-10-353-690-12
17	1472	64.9	431	5	US-10-756-149-5279
18	1472	64.9	431	6	US-11-044-570-2
19	1468	64.7	431	3	US-09-810-808-5
20	1458.5	64.3	430	3	US-09-810-808-9
21	1447	63.8	594	5	US-10-732-923-10768
22	1415	62.4	388	4	US-10-131-410-104
23	1414	62.3	433	5	US-10-732-923-10767
24	1346.5	59.3	340	4	US-10-217-574-17
25	1346.5	59.3	340	4	US-10-217-555-17
26	1338	59.0	276	3	US-09-764-868-669
27	1338	59.0	276	3	US-09-764-875-1176

28	1329.5	58.6	382	4	US-10-296-115-1109
29	1329	58.6	396	5	US-10-926-543-83
30	1328.5	58.6	427	5	US-10-753-267-126
31	1323.5	58.3	367	3	US-09-971-118-2
32	1323.5	58.3	367	4	US-10-291-172-256
33	1323.5	58.3	367	4	US-10-429-160-52
34	1323.5	58.3	367	4	US-10-221-278-256
35	1323.5	58.3	367	4	US-10-380-235-6
36	1187.5	52.3	308	4	US-10-664-421-85
37	1187.5	52.3	308	5	US-10-941-635-85
38	1171	51.6	398	4	US-10-262-511-140
39	1047	46.1	194	3	US-09-784-249-4
40	1019.5	44.9	422	4	US-10-369-493-7027
41	976	43.0	276	3	US-09-764-868-811
42	976	43.0	276	3	US-09-764-875-1050
43	870	38.3	465	3	US-09-526-043-2
44	870	38.3	465	4	US-10-394-568-2
45	870	38.3	465	4	US-10-394-568-12

ALIGNMENTS

RESULT 1

US-10-295-027-116
; Sequence 116, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-116

Query Match 100.0%; Score 2269; DB 4; Length 429;

Best Local Similarity 100.0%; Pred. No. 3.5e-172;			
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLYVRPELYNHPDVFRAFLQMDSPKHQSD	60
Db	1	MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLYVRPELYNHPDVFRAFLQMDSPKHQSD	60
QY	61	PSEDEDRSSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLQDKF	120
Db	61	PSEDEDRSSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLQDKF	120
QY	121	YAVKVLQKKIVLNARKEQKHMAERNVLLKNVGHFPLVGLHYSFQTTTEKLYFVLDFVNGGE	180
Db	121	YAVKVLQKKIVLNARKEQKHMAERNVLLKNVGHFPLVGLHYSFQTTTEKLYFVLDFVNGGE	180
QY	181	LFPHLQERSFPEHRARFYAAETASALGYLHSIKIVYRDILKPENILDSVGHVVLTDFGL	240
Db	181	LFPHLQERSFPEHRARFYAAETASALGYLHSIKIVYRDILKPENILDSVGHVVLTDFGL	240
QY	241	CKEGIAISDTTTFCGTPEYLAPEVIRKQPDVNTVDMWCLGAVLYEMLYGLPPFYCRDVA	300
Db	241	CKEGIAISDTTTFCGTPEYLAPEVIRKQPDVNTVDMWCLGAVLYEMLYGLPPFYCRDVA	300
QY	301	EMYDNILHKPLSRPGVSLTAWSTLEELLEKORNLGAKEDFLEIQNHPPFESLSWADL	360
Db	301	EMYDNILHKPLSRPGVSLTAWSTLEELLEKORNLGAKEDFLEIQNHPPFESLSWADL	360
QY	361	VOKKIPPPNPNVAGPDIDRFDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY	420
Db	361	VOKKIPPPNPNVAGPDIDRFDTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY	420
QY	421	APPSDDLFL 429	
Db	421	APPSDDLFL 429	
RESULT 2			
US-09-764-875-746			
; Sequence 746, Application US/09764875			
; Publication No. US20040018969A1			
; GENERAL INFORMATION:			
; APPLICANT: Rosen et al.			
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
; FILE REFERENCE: P0202			
; CURRENT APPLICATION NUMBER: US/09/764,875			
; CURRENT FILING DATE: 2001-01-17			
; Prior application data removed - consult PALM or file wrapper			
; NUMBER OF SEQ ID NOS: 1249			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 746			
; LENGTH: 496			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; US-09-764-875-746			
Query Match 100.0%; Score 2269; DB 3; Length 496;			
Best Local Similarity 100.0%; Pred. No. 4.1e-172;			
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLYVRPELYNHPDVFRAFLQMDSPKHQSD	60
Db	68	MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLYVRPELYNHPDVFRAFLQMDSPKHQSD	127
QY	61	PSEDEDRSSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLQDKF	120
Db	128	PSEDEDRSSQKLHSTSQNLGPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLQDKF	187
QY	121	YAVKVLQKKIVLNARKEQKHMAERNVLLKNVGHFPLVGLHYSFQTTTEKLYFVLDFVNGGE	180
Db	188	YAVKVLQKKIVLNARKEQKHMAERNVLLKNVGHFPLVGLHYSFQTTTEKLYFVLDFVNGGE	247
QY	181	LFPHLQERSFPEHRARFYAAETASALGYLHSIKIVYRDILKPENILDSVGHVVLTDFGL	240

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; Sequence 4, Application US/10737450
; Publication No. US20040235071A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Ecsedy, Jeffrey A.
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tighe Nestor, Michelle
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 15986, 2188, 20743, 9148, 9151, 9791, 44252,
; TITLE OF INVENTION: 14184, 8204, 7970, 25552, 21657, 26492, 2411, 15088,
; TITLE OF INVENTION: 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694,
; TITLE OF INVENTION: 15701, 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201,
; TITLE OF INVENTION: 6985, 9883, 12238, 18057, 21617, 39228, 49928, 54476, 62113,
; TITLE OF INVENTION: 64316, 12264, 32362, 58198, 2887, 3205, 8557, 9600, 9693,
; TITLE OF INVENTION: 44867, 53058, 55556, 57658, 2208, 10252, 10302, 14218,
; TITLE OF INVENTION: 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827, 21708,
; FILE REFERENCE: MP102-207P1RNMNM
; CURRENT APPLICATION NUMBER: US/10737,450
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/435,108
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/436,443
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/438,498
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/444,370
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/446,031
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/453,635
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/457,199
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/462,458
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/466,732
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/469,184
; PRIOR FILING DATE: 2003-05-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-737-450-4

Query Match 100.0%; Score 2269; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 4.1e-172;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
Db 68 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127

QY 61 PSEDEDESSQKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 120
Db 128 PSEDEDESSQKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 187

QY 121 YAVKVLQKKIIVLNKKEQKHIAMERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 180
Db 188 YAVKVLQKKIIVLNKKEQKHIAMERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 247

QY 181 LFFHLQERSFPEHRARFYAAETASALGYLHSIKIIVYRDLKPNILLDSVGHVVLDTDFGL 240
Db 248 LFFHLQERSFPEHRARFYAAETASALGYLHSIKIIVYRDLKPNILLDSVGHVVLDTDFGL 307

QY 241 CKEGTAISDTTTCGTPEYLAPEVIRKOPYNTVDWMCGLGAVLYEMLYGLPFPYCRDVA 300
Db 308 CKEGTAISDTTTCGTPEYLAPEVIRKOPYNTVDWMCGLGAVLYEMLYGLPFPYCRDVA 367

QY 301 EMYDNILHKPLSLRPGVSLTAMSIELLELEKDRQNLGAKEDFLEIQNHPPFFESLSWADL 360
Db 368 EMYDNILHKPLSLRPGVSLTAMSIELLELEKDRQNLGAKEDFLEIQNHPPFFESLSWADL 427

QY 361 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db 428 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487

RESULT 5
US-09-784-249-2
; Sequence 2, Application US/09784249
; Patent No. US20010027184A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Kumar
; TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE (H-SGK2)
; FILE REFERENCE: GH-70124-C1
; CURRENT APPLICATION NUMBER: US/09/784,249
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 08/997,212
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/051,446
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-784-249-2

Query Match 99.7%; Score 2263; DB 3; Length 496;
Best Local Similarity 99.8%; Pred. No. 1.2e-171;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
Db 68 MALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127

QY 61 PSEDEDESSQKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 120
Db 128 PSEDEDESSQKLHSTSONINLGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKGKF 187

QY 121 YAVKVLQKKIIVLNKKEQKHIAMERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 180
Db 188 YAVKVLQKKIIVLNKKEQKHIAMERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 247

QY 181 LFFHLQERSFPEHRARFYAAETASALGYLHSIKIIVYRDLKPNILLDSVGHVVLDTDFGL 240
Db 248 LFFHLQERSFPEHRARFYAAETASALGYLHSIKIIVYRDLKPNILLDSVGHVVLDTDFGL 307

QY 241 CKEGTAISDTTTCGTPEYLAPEVIRKOPYNTVDWMCGLGAVLYEMLYGLPFPYCRDVA 300
Db 308 CKEGTAISDTTTCGTPEYLAPEVIRKOPYNTVDWMCGLGAVLYEMLYGLPFPYCRDVA 367

QY 301 EMYDNILHKPLSLRPGVSLTAMSIELLELEKDRQNLGAKEDFLEIQNHPPFFESLSWADL 360
Db 368 EMYDNILHKPLSLRPGVSLTAMSIELLELEKDRQNLGAKEDFLEIQNHPPFFESLSWADL 427

QY 361 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db 428 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487
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QY 421 APPSEDLFL 429
DB 488 APPSEDLFL 496

RESULT 6
US-10-755-889-42
; Sequence 42, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-42

Query Match 99.0%; Score 2246; DB 4; Length 496;
Best Local Similarity 99.1%; Pred. No. 2.8e-170; Mismatches 3; Indels 0; Gaps 0;
Matches 425; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKORRAGINEFIQNLVRPELYNHPDVRAFLQMDSPKQSD 60
DB 68 MALKIPAKRIFGDNFDPDFIKORRAGINEFIQNLVRPELYNHPDVRAFLQMDSPKQSG 127
QY 61 PSEDEDESSQKLHSTSQNLINLPGSGNPHAKPTDFDLKVGKSGFKVLLAKRKLDGKF 120
DB 128 PSEDEDESSQKLHSTSQNLINLPGSGNPHAKPTDFDLKVGKSGFKVLLAKRKLDGKV 187
QY 121 YAVKVLQKKIVLNKQKQKIMAEARNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
DB 188 YAVKVLQKKIVLNKQKQKIMAEARNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 247
QY 181 LPFHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVVLDFGL 240
DB 248 LPFHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVVLDFGL 307
QY 241 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
DB 308 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVA 367
QY 301 EMDYNTILHKPLSLRPGVSLTAWLSILBELLEKQRNRLGAKEDFLEIQNHPPFESLSWADL 360
DB 368 EMDYNTILHKPLSLRPGVSLRWSILBELLEKQRNRLGAKEDFLEIQNHPPFESLSWADL 427
QY 361 VQKKIPIPPNPVAGPDDIRNFDATAETEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
DB 428 VQKKIPIPPNPVAGPDDIRNFDATAETEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487
QY 421 APPSEDLFL 429
DB 488 APPSEDLFL 496

RESULT 7
US-10-094-749-1861
; Sequence 1861, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
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; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1861
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1861

Query Match 66.2%; Score 1501; DB 4; Length 526;
Best Local Similarity 66.8%; Pred. No. 6.6e-111;
Matches 286; Conservative 52; Mismatches 76; Indels 14; Gaps 3;

QY 6 PAKRIFGDNFDPDFIKORRAGINEFIQNLVRPELYNHPDVRAFLQMDSPKH----QSDP 61
DB 109 PDPRTFTWNTDDPAFMKQRRMGLNDFIQTIANNYSYACKHPDEVOSILKISQPEPELMNANP 168
QY 62 SDEDEDESSQKLHSTSQNLINLPGSGNPHAKPTDFDLKVGKSGFKVLLAKRKLDGKFY 121
DB 169 SPPP-----SPSQINLPGSSNPHAKPSDFHFLKVGSGFKVLLARHKAEEVFY 219
QY 122 AVKVLQKKIVLNKQKQKIMAEARNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGEL 181
DB 220 AVKVLQKKAILKKBEKHMISERNVLLKNVHPFLVGLHFSFQTADKLYFVLDIYINGGEL 279
QY 182 PFHLQERSFPFHRARFYAAETASALGYLHSIKIVYRDLKPNILLDSVGHVVLTDGFLC 241
DB 280 FYHLQERCFLEPRARFYAAETASALGYLHSUNIYVRDLKPNILLDSQGHIVLTDGFLC 339
QY 242 KEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVAE 301
DB 340 KENIEHNSTSTFCGTGTPPEYLAPEVHLKQPDYRDTVDWCLGAVLYEMLYGLPPFYSRTAE 399
QY 302 MYDNTILHKPLSLRPGVSLTAWLSILBELLEKQRNRLGAKEDFLEIQNHPPFESLSWADLV 361
DB 400 MYDNTILNKPLQLKPNITNSARHLLGELLQKDRTKRLGAKDDFMEIKSHVFFSFLINWDDLI 459
QY 362 OKKIPIPPNPVAGPDDIRNFDATAETEETVPYSCVSSDYSIVNASVLEADDAFVGFSYA 421
DB 460 NKKITPPFPNPVSGPNDLRHFDPEETEEPVPNSIGKSPDSVLVTASVKRAAEAFVGFSYA 519
QY 422 PPSEDLFL 429
DB 520 PPT-DSFL 526

RESULT 8
US-10-067-977-4
; Sequence 4, Application US/10067977
; Publication No. US20030157679A1
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GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-4

Query Match 65.1%; Score 1476; DB 4; Length 407;
Best Local Similarity 67.5%; Pred. No. 4.7e-109;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
QY 19 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 74
DB 3 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 53
QY 75 STSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVKVLQKIVLNR 134
DB 54 SPSQOINLGPSSNPHAKPSDFHFLKVIKGSFGKVLAKRKLKDGKFAVKVLQKIVLNR 113
QY 135 KEQKHMAERNVLLKNVHPFLVGLHYSFQTEKLYFVLDVNGGELFFHLQERSPEH 194
DB 114 KEEKHIMSERVLLKNVHPFLVGLHYSFQTEKLYFVLDVNGGELFFHLQERSPEH 173
QY 195 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254
DB 174 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 233
QY 255 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 314
DB 234 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 293
QY 315 PGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFESLSWADLVQKIPPPFNVA 374
DB 294 PNITNSARHLLEGLLQKDRKRLGAKEDFLEIQNHPPFESLSWADLVQKIPPPFNVA 353
QY 375 GPDIRNFDFTAEETVPYSCVSSDYISVNASVLEADDAFVGFYSYAPPSDELFL 429
DB 354 GPDLRHFDFEETPEVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPT-DSFL 407

RESULT 9
US-10-827-272-4
; Sequence 4, Application US/10827272
; Publication No. US20040203127A1
; GENERAL INFORMATION:
; APPLICANT: KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001313-DIV
; CURRENT APPLICATION NUMBER: US/10/827,272
; CURRENT FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-827-272-4

Query Match 65.1%; Score 1476; DB 4; Length 407;
Best Local Similarity 67.5%; Pred. No. 4.7e-109;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 74
DB 3 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 53
QY 75 STSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVKVLQKIVLNR 134
DB 54 SPSQOINLGPSSNPHAKPSDFHFLKVIKGSFGKVLAKRKLKDGKFAVKVLQKIVLNR 113
QY 135 KEQKHMAERNVLLKNVHPFLVGLHYSFQTEKLYFVLDVNGGELFFHLQERSPEH 194
DB 114 KEEKHIMSERVLLKNVHPFLVGLHYSFQTEKLYFVLDVNGGELFFHLQERSPEH 173
QY 195 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254
DB 174 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 233
QY 255 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 314
DB 234 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 293
QY 315 PGVSLTAWSLLELLEKQDNRLGAKEDFLEIQNHPPFESLSWADLVQKIPPPFNVA 374
DB 294 PNITNSARHLLEGLLQKDRKRLGAKEDFLEIQNHPPFESLSWADLVQKIPPPFNVA 353
QY 375 GPDIRNFDFTAEETVPYSCVSSDYISVNASVLEADDAFVGFYSYAPPSDELFL 429
DB 354 GPDLRHFDFEETPEVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPT-DSFL 407

RESULT 10
US-09-981-353-7
; Sequence 7, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Laeek, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1
US-09-981-353-7

Query Match 65.1%; Score 1476; DB 3; Length 431;
Best Local Similarity 67.5%; Pred. No. 5.1e-109;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
QY 19 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 74
DB 27 FIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQWDSPKH---QSDPSEDEDESSQKLH 77
QY 75 STSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFAVKVLQKIVLNR 134
DB 78 SPSQOINLGPSSNPHAKPSDFHFLKVIKGSFGKVLAKRKLKDGKFAVKVLQKIVLNR 137
QY 135 KEQKHMAERNVLLKNVHPFLVGLHYSFQTEKLYFVLDVNGGELFFHLQERSPEH 194
DB 138 KEEKHIMSERVLLKNVHPFLVGLHYSFQTEKLYFVLDVNGGELFFHLQERSPEH 197
QY 195 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254
DB 198 RARFYAAETASALGYLHSLNIVRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 257
QY 255 CGTPEYLAPEVIRKQPDYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLR 314

Db 258 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPPYSRNTAEMVDNINLKPQLK 317
Qy 315 PGVSLTAMSI LLEKDRQNRILGAKEDFLEIQNHPPFESLSWADLVQKKIPPPNPVA 374
Db 318 PNITNSARHLLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLLINKKITPPFPNPVS 377
Qy 375 GPDDIRNFDTATTEETVPYSCVSSDYSIVNASVLEADDAFVGFSYAPPSDELFL 429
Db 378 GPNDLRHDFDEFTPEEPVNSIGKSPDSVLVTASVKEAAEAFUGFSYAPPT-DSFL 431

RESULT 11
US-10-403-161-2
; Sequence 2, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-2

Query Match 65.1%; Score 1476; DB 4; Length 431;
Best Local Similarity 67.5%; Pred. No. 5.1e-109;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
Qy 19 FIKORRAGLNERIQNLVRYPELVNHPDVRAFLQMDSPKH----QSDPSDEDESSQKLH 74
Db 27 FMKQRMGLNDFIQKIANNYSACKHEVQSILKISQPEPELMNANPSPPP----- 77
Qy 75 STSQINILGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKFYAVKVLQKTVLNR 134
Db 78 SPQQINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKK 137
Qy 135 KEQKHMAERNVLLKNVHPFLVGLHYSFOTTEKLYFVLDVFNNGELFFHLQERSFPEH 194
Db 138 KEEKHIMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFFHLQERCFLP 197
Qy 195 RARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDVFGCKEGIAISDTTTF 254
Db 198 RARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHVILVTDVFGCKENIENSTTSTF 257
Qy 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVAEMVDNINLHKPLSLR 314
Db 258 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPPYSRNTAEMVDNINLKPQLK 317

Qy 315 PGVSLTAMSI LLEKDRQNRILGAKEDFLEIQNHPPFESLSWADLVQKKIPPPNPVA 374
Db 318 PNITNSARHLLEGLLQKDRKRLGAKDDFMEIKSHVFFSLINWDDLLINKKITPPFPNPVS 377
Qy 375 GPDDIRNFDTATTEETVPYSCVSSDYSIVNASVLEADDAFVGFSYAPPSDELFL 429
Db 378 GPNDLRHDFDEFTPEEPVNSIGKSPDSVLVTASVKEAAEAFUGFSYAPPT-DSFL 431

RESULT 12
US-10-403-161-4
; Sequence 4, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-4

Query Match 65.1%; Score 1476; DB 4; Length 431;
Best Local Similarity 67.5%; Pred. No. 5.1e-109;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
Qy 19 FIKORRAGLNERIQNLVRYPELVNHPDVRAFLQMDSPKH----QSDPSDEDESSQKLH 74
Db 27 FMKQRMGLNDFIQKIANNYSACKHEVQSILKISQPEPELMNANPSPPP----- 77
Qy 75 STSQINILGPSGNPHAKPTDFDLKVIKGSFGKVLAKRKLKDKFYAVKVLQKTVLNR 134
Db 78 SPQQINLGPSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKK 137
Qy 135 KEQKHMAERNVLLKNVHPFLVGLHYSFOTTEKLYFVLDVFNNGELFFHLQERSFPEH 194
Db 138 KEEKHIMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFFHLQERCFLP 197
Qy 195 RARFYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDVFGCKEGIAISDTTTF 254
Db 198 RARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHVILVTDVFGCKENIENSTTSTF 257
Qy 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVAEMVDNINLHKPLSLR 314
Db 258 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPPYSRNTAEMVDNINLKPQLK 317

QY 315 PGVSLTAWSLLELEKDRQNRGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374
Db 318 PNITNSARHLLEGLQKDRTKRLGAKODFMEIKSHVFFSLINWDDLKINKITPPFPNVS 377
QY 375 GPDIRNFDTAFTETVPYSCVSSDIYVNASVLEADDAFVGFSYAPPSDELFL 429
Db 378 GPNDLRHDFEFTPEEPVNSIGKSPDSVLVTASVKEAAEAPLGFYSAPPT-DSFL 431

RESULT 13

US-10-067-977-2
; Sequence 2, Application US/10067977
; Publication No. US20030157679A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-2

Query Match 65.1%; Score 1476; DB 4; Length 445;
Best Local Similarity 67.5%; Pred. No. 5.3e-109;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKORAGLNEFTQNLVRYPELVNHPDVRAFLQWDSFKH---QSDPSEDESSQKLH 74
Db 41 FMKQRRMGLNDFLOKIANNSYACKHPEVQSIKISQPEPELMNANSPPPP----- 91
QY 75 STSQINLPGSGNPHAKPTDFELKVIKGSFGKVLAKRKLDGKFYAVKVLQKKIVLNR 134
Db 92 SPQQINLGPSSNPHAKPSDFELKVIKGSFGKVLAKRKLDGKFYAVKVLQKKAILKK 151
QY 135 KEOKHIMAEARNVLLKNVHPFLVGLHYSPOTTBKLIFVLDVNGGELFFHLQERSFPEH 194
Db 152 KEEKHIMSERNVLLKNVHPFLVGLHYSPOTTBKLIFVLDVNGGELFFHLQERSFPEH 211
QY 195 RARFYAAETASALGYLHSIKIVYRDLKPNILDSQGHIVLTDGFLCKENIENSTTSTF 254
Db 212 RARFYAAETASALGYLHSIKIVYRDLKPNILDSQGHIVLTDGFLCKENIENSTTSTF 271
QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYCRDVAEMVDNILHKPLSLR 314
Db 272 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYCRDVAEMVDNILHKPLSLR 331
QY 315 PGVSLTAWSLLELEKDRQNRGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374
Db 332 PNITNSARHLLEGLQKDRTKRLGAKODFMEIKSHVFFSLINWDDLKINKITPPFPNVS 391
QY 375 GPDIRNFDTAFTETVPYSCVSSDIYVNASVLEADDAFVGFSYAPPSDELFL 429
Db 392 GPNDLRHDFEFTPEEPVNSIGKSPDSVLVTASVKEAAEAPLGFYSAPPT-DSFL 445

RESULT 14

US-10-827-272-2
; Sequence 2, Application US/10827272
; Publication No. US20040203127A1
; GENERAL INFORMATION:
; APPLICANT: KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001313-DIV
; CURRENT APPLICATION NUMBER: US/10/827,272

; CURRENT FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-827-272-2

Query Match 65.1%; Score 1476; DB 4; Length 445;
Best Local Similarity 67.5%; Pred. No. 5.3e-109;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKORAGLNEFTQNLVRYPELVNHPDVRAFLQWDSFKH---QSDPSEDESSQKLH 74
Db 41 FMKQRRMGLNDFLOKIANNSYACKHPEVQSIKISQPEPELMNANSPPPP----- 91
QY 75 STSQINLPGSGNPHAKPTDFELKVIKGSFGKVLAKRKLDGKFYAVKVLQKKIVLNR 134
Db 92 SPQQINLGPSSNPHAKPSDFELKVIKGSFGKVLAKRKLDGKFYAVKVLQKKAILKK 151
QY 135 KEOKHIMAEARNVLLKNVHPFLVGLHYSPOTTBKLIFVLDVNGGELFFHLQERSFPEH 194
Db 152 KEEKHIMSERNVLLKNVHPFLVGLHYSPOTTBKLIFVLDVNGGELFFHLQERSFPEH 211
QY 195 RARFYAAETASALGYLHSIKIVYRDLKPNILDSQGHIVLTDGFLCKENIENSTTSTF 254
Db 212 RARFYAAETASALGYLHSIKIVYRDLKPNILDSQGHIVLTDGFLCKENIENSTTSTF 271
QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYCRDVAEMVDNILHKPLSLR 314
Db 272 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPYCRDVAEMVDNILHKPLSLR 331
QY 315 PGVSLTAWSLLELEKDRQNRGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374
Db 332 PNITNSARHLLEGLQKDRTKRLGAKODFMEIKSHVFFSLINWDDLKINKITPPFPNVS 391
QY 375 GPDIRNFDTAFTETVPYSCVSSDIYVNASVLEADDAFVGFSYAPPSDELFL 429
Db 392 GPNDLRHDFEFTPEEPVNSIGKSPDSVLVTASVKEAAEAPLGFYSAPPT-DSFL 445

RESULT 15

US-10-000-039-2
; Sequence 2, Application US/10000039
; Publication No. US20030003559A1
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/000,039
; FILING DATE: 04-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:32:16 ; Search time 11.0623 Seconds
(without alignments)
419.957 Million cell updates/sec

Title: US-09-868-131A-4

Perfect score: 2269

Sequence: 1 MALKIPAKRIFGDNFDPDFI.....EADDAFGVFSYAPPSDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1501	66.2	543	6	US-10-821-234-1158
2	816.5	36.0	480	7	US-11-109-156-18
3	786	34.6	495	6	US-10-770-726-81
4	779.5	34.4	737	7	US-11-152-366-28
5	708	31.2	740	6	US-10-878-556A-129
6	686.5	30.3	705	6	US-10-995-561-856
7	686.5	30.3	706	6	US-10-995-561-855
8	686.5	30.3	706	6	US-11-099-958-1
9	684.5	30.2	351	7	US-11-099-958-2
10	684	30.1	942	6	US-10-770-726-76
11	657.5	29.0	398	7	US-11-132-142-7
12	654.5	28.8	341	7	US-11-092-168-4
13	650	28.6	351	7	US-11-132-142-13
14	649	28.6	381	7	US-11-132-142-9
15	647.5	28.5	351	7	US-11-132-142-14
16	647	28.5	343	7	US-11-092-168-3
17	642	28.3	480	7	US-11-132-142-6
18	641.5	28.3	515	7	US-11-132-142-8
19	637.5	28.1	462	7	US-11-132-142-10
20	635.5	28.0	350	6	US-10-497-767-4
21	632	27.9	395	7	US-11-132-142-12
22	626.5	27.6	353	7	US-11-132-142-11
23	624.5	27.5	548	7	US-11-132-142-5
24	543	23.9	1732	6	US-10-055-877-147
25	534	23.5	1590	6	US-10-055-877-146

ALIGNMENTS

RESULT 1

US-10-821-234-1158
; Sequence 1158, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1158
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1158

Query Match 66.2%; Score 1501; DB 6; Length 543;
Best Local Similarity 66.8%; Pred. No. 1.4e-126;
Matches 286; Conservative 52; Mismatches 76; Indels 14; Gaps 3;
QY 6 PAKRIFGDNFDPDFIKORAGLNEFTQNLVRYPELVNHPDVRFLQWDSPKH----QSDP 61
Db 126 PDPRTWTNDDPAFMQRMGLNDFIQKIANNSSACKHEVQSILKISQBPPELMNANP 185
QY 62 SEDEDRSSQKLHSTQNTNLGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLCKFY 121
Db 186 SPPP-----SPSQNLGPNPHAKPSDFHLKVIKGSFGKVLARHAKBEVFY 236
QY 122 AVKLQKIVLNKKEOKHMAERNVLLKNVHPFLVGLHYSFOTTEKLYFVLDPVNGGEL 181
Db 237 AVKLQKAILKXKEKHIMSENVLLKNVHPFLVGLHFSFOTADKLYFVLDTYNGGEL 296
QY 182 FFHLQERSFPBHRARFAAEIASALGYLHSIKIVYRDLKPNENILDSVGHVVLTDGFLC 241
Db 297 FFHLQERCFLEPRARFAAEIASALGYLHSINIVYRDLKPNENILDSQGHIVLTDGFLC 356
QY 242 KEGIALSDTTTTTCGTPPEYLAPEVTRKQYDNTVDMWCLGAVLYEMLYGLPPYCRDVAE 301
Db 357 KENIEHNSTSTFCGTPPEYLAPEVTRKQYDNTVDMWCLGAVLYEMLYGLPPYCRDVAE 416
QY 302 MYDNILHKLPLSLRPGVSLTAWSTLELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLV 361

Db 417 MYDNLKPLQAPNTNSARHLEGLQKDRYRKGAKDDFWEIKSHVFFSLINWDDLI 476
QY 362 QKKIPFPNPNVAGPDDIRNFDTAFTETVPYGVCSVSSDYSIVNASVLEADDAFVGFSYA 421
Db 477 NKKITPFPNPNVSGPNDLRHFDPEFTTEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYA 536

QY 422 PPSDELFL 429
Db 537 PPT-DSFL 543

RESULT 2

US-11-109-156-18

; Sequence 18, Application US/11109156
; Publication No. US20050250144A1

; GENERAL INFORMATION:

; APPLICANT: Toshio Ota

; APPLICANT: Takao Isegai

; APPLICANT: Tetsuo Nishikawa

; APPLICANT: Koji Hayashi

; APPLICANT: Kaoru Otsuka

; APPLICANT: Jun-Ichi Yamamoto

; APPLICANT: Shizuko Ishii

; APPLICANT: Tomoyasu Sugiyama

; APPLICANT: Ai Wakamatsu

; APPLICANT: Keiichi Nagai

; APPLICANT: Tetsuji Otsuki

; APPLICANT: Shin-Ichi Funahashi

; APPLICANT: Chiaki Senoo

; APPLICANT: Jun-Ichi Nezu

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN

; FILE REFERENCE: 06501-039002

; CURRENT APPLICATION NUMBER: US/11/109,156

; CURRENT FILING DATE: 2005-04-19

; PRIOR APPLICATION NUMBER: US/10/060,065

; PRIOR FILING DATE: 2002-01-29

; PRIOR APPLICATION NUMBER: PCT/JP00/05061

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/159,590

; PRIOR FILING DATE: 1999-10-18

; PRIOR APPLICATION NUMBER: US 60/183,322

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: JP 11-248036

; PRIOR FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: JP 2000-118776

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: JP 2000-183767

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: JP 2000-241899

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 480

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-109-156-18

Query Match 36.0%; Score 816.5; DB 7; Length 480;
Best Local Similarity 41.0%; Pred. No. 1.9e-65;
Matches 185; Conservative 63; Mismatches 146; Indels 57; Gaps 12;

QY 17 PDFIKORRAGNEFIQNLVRYPELY--NHPDVRAFL-----QMDSPKHQSDPSEDED 66
Db 42 PQVDQREAPLNNF---SVAQCQLMKTERPRNPTFIIRCLQWTTVIERTFHVETPEERE 98
QY 67 ERSS-----QKLHSTSONINLG-PSGNPH-----AKP-----TDFDFLKVGK 103
Db 99 WTTAIQTVDGLKKQEEEMDFRSGSPSDNSGAEEMVSLAKPKHRVTWNEFEYLKLLGK 158
QY 104 GSGFKVLLAKRKLDGKFYAVKVLQKKIVLNRKEQKHMAERNVLLKNVKHPFLVGLHYSF 163

Db 159 GTFGKVLVKEATGRYVAMKILKKEVIVAKDEVANTLTE--NRVLQNSRHPPFTALKYSP 217
QY 164 QTTEKLYFVLDVFNVGSELFPHLQRRSFPEHRARFYAAEIASALGYLHSHIK-IYVRDLKP 222
Db 218 QTHDRLCFVMEYANGSELFPHLSRERVFSSEDRARFYGAELVSALDYLVHSEKNVYRDLXL 277
QY 223 ENILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYLAPVIRKQPDYNTVDWVCLGA 282
Db 278 ENMLDKDGHIIKITDFGLCKEGIKDGAATMKTCGTPPEYLAPVLENDNDYGRAVDWVGLGV 337
QY 283 VLYEMLYGLPPFYCRDVAEMYNILHKLPLSLRPGVSLTAWLSILEELLEKDRNRL--GAKE 341
Db 338 VMYEMMCGRLPPYNDHEKLFELILMEEIRFRFTLGPEAKSLSLGLLKKDKPKORLGGSE 397
QY 342 DFLEIQNHPPFESLSWADLVQKKIPFPNPNVAGPDDIRNFDTAFTETVPYS----- 394
Db 398 DAKIEMQHRFFAGIVQHVVEKKLSPPFKPQVTSSETDTRVDFDEFTAQMITTPPDQDDS 457
QY 395 -VCVSSDYSIVNASVLEADDAFVGFSYAPPS 424
Db 458 MECVDS-----ERRPFPQFSYSASS 478

RESULT 3

US-10-770-726-81

; Sequence 81, Application US/10770726

; Publication No. US20050266409A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Brown, Eugene

; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATIN

; FILE REFERENCE: AM101079 (031896-010000)

; CURRENT APPLICATION NUMBER: US/10/770,726

; CURRENT FILING DATE: 2004-02-04

; NUMBER OF SEQ ID NOS: 48640

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 81

; LENGTH: 495

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-770-726-81

Query Match 34.6%; Score 786; DB 6; Length 495;
Best Local Similarity 42.1%; Pred. No. 1.1e-62;
Matches 170; Conservative 70; Mismatches 124; Indels 40; Gaps 11;

QY 48 AFLQWDSPKHQSDPSEDEDESS-----QKLHSTSONINLGPSG- 86
Db 16 AVFDLDELTEGSEGEPELSPADACPLAELRAAGLEPVGHYEVELTETSVNVGPRI 75
QY 87 NPHAKPTDFDLKVIKGSFGKVLAKRKLD---GKFYAVKVLQK-KIVLNRKEQKHIM 141
Db 76 GPHC-----FELLRVLGKGGYGVQV-RKVGQTNLGIYAMKVLRAKIVRNAKDTAHR 130
QY 142 AERNVLLKNVKHPFLVGLHYSQTTEKLYFVLDVFNVGSELFPHLQRRSFPEHRARFYAA 201
Db 131 ASRNT-LESVKHPFVELAYAFQTGGKLYLLECLSGGSELFTHLEREGIFLEDTACFYLA 189
QY 202 ETASALGYLHSHIKIVYRDLKPNILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYL 261
Db 190 EITLALGHLHSGIIVYRDLKPNINILMSQGHKLDTDFGLCKESIHEGAVTHTCGTIEYM 249
QY 262 APEVIRKQPDYNTVDWVCLGAVLYEMLYGLPPFYCRDVAEMYNILHKLPLSLRPGVSLTA 321
Db 250 APEILVRSCHNRADVWSIGALMYDMLTGTSPFTAENRKKTKMDKIIRGKALAPPLYLTPDA 309
QY 322 WSILEELLEKDRNRL--GAKEDFLEIQNHPPFESLSWADLVQKKIPFPNPNVAGPDDIR 380
Db 310 RDLVKKFLKRNPSQRIGGGGGAADVQRHPPFRHNMWDDLAWRVDPFPRPCLQSBEDVS 369


```
; Publication No. US20060003431A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Zhang Bao
; APPLICANT: Olland, Stephanie
; APPLICANT: Wolfstrom, Scott
; APPLICANT: Malakian, Karl
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Lee, Julie
; APPLICANT: Fitz, Lori
; APPLICANT: Greco, Rita
; APPLICANT: Chaudhary, Divya
; APPLICANT: Somers, William Stuart
; APPLICANT: Mosyak, Lidia
; TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
; FILE REFERENCE: 16163-018001
; CURRENT APPLICATION NUMBER: US/11/099,958
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/560,441
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-099-958-2

Query Match      30.2%; Score 684.5; DB 7; Length 351;
Best Local Similarity 41.9%; Pred. No. 7.8e-54;
Matches 143; Conservative 62; Mismatches 125; Indels 11; Gaps 5;

QY 84 PSGNPHAKPTDFDLKVIKGSFGKVLAKKLDGKFAVAVKVLQKIVLNKKEQKHMAE 143
DB 8 PSQIKLIKIEDFILHRLMKGSGKGFVLAFFKTNQFAIKALKKOVLMDDDDVECTMVE 67

QY 144 RNVLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQERSFPEHRAFYAAEI 203
DB 68 KRVLSLAWEHPFLTHMECTFQTKENLFFVMEYLNGDGLMYHIQSKHFDLSRATFYAAEI 127

QY 204 ASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEVLAP 263
DB 128 ILGLQFLHSGIVYRDLKPNILLDKDGHKIADFGMCKENMLGDAKNTNFCGTPDYIAP 187

QY 264 EVIRKQYDNTVDWMCGLGAVLYEMLYGLPPFYCRDVAEMYDNI-LHKPLSLRPGVSLTAW 322
DB 188 EILGQKYNHSDVMSFGVLLYEMLYGSPFHGQDEELFHSIRMDNPFYPR-WLEKEAK 246

QY 323 SILLELEKQRNLGAKEDFLEIQNHPPFESLWADLVQKIPPPPNVAGPDDIRNF 382
DB 247 DLLVKLFVREPEKRLVGRGD--LRQHPLEINWELEKEIDPPPRPKVSPFFDCSNF 303

QY 383 DTAFTETVYSCVSDSYDINVASVLEADDAFVGFSYAPP 423
DB 304 DKEFLNEKPLSLF---ADRALINSM---DQNMFRNFSFMNP 338

RESULT 10
US-10-770-726-76
; Sequence 76, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76

; Publication No. US20060003431A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Zhang Bao
; APPLICANT: Olland, Stephanie
; APPLICANT: Wolfstrom, Scott
; APPLICANT: Malakian, Karl
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Lee, Julie
; APPLICANT: Fitz, Lori
; APPLICANT: Greco, Rita
; APPLICANT: Chaudhary, Divya
; APPLICANT: Somers, William Stuart
; APPLICANT: Mosyak, Lidia
; TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
; FILE REFERENCE: 16163-018001
; CURRENT APPLICATION NUMBER: US/11/099,958
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/560,441
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-099-958-2

Query Match      30.2%; Score 684.5; DB 7; Length 351;
Best Local Similarity 41.9%; Pred. No. 7.8e-54;
Matches 143; Conservative 62; Mismatches 125; Indels 11; Gaps 5;

QY 84 PSGNPHAKPTDFDLKVIKGSFGKVLAKKLDGKFAVAVKVLQKIVLNKKEQKHMAE 143
DB 8 PSQIKLIKIEDFILHRLMKGSGKGFVLAFFKTNQFAIKALKKOVLMDDDDVECTMVE 67

QY 144 RNVLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQERSFPEHRAFYAAEI 203
DB 68 KRVLSLAWEHPFLTHMECTFQTKENLFFVMEYLNGDGLMYHIQSKHFDLSRATFYAAEI 127

QY 204 ASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEVLAP 263
DB 128 ILGLQFLHSGIVYRDLKPNILLDKDGHKIADFGMCKENMLGDAKNTNFCGTPDYIAP 187

QY 264 EVIRKQYDNTVDWMCGLGAVLYEMLYGLPPFYCRDVAEMYDNI-LHKPLSLRPGVSLTAW 322
DB 188 EILGQKYNHSDVMSFGVLLYEMLYGSPFHGQDEELFHSIRMDNPFYPR-WLEKEAK 246

QY 323 SILLELEKQRNLGAKEDFLEIQNHPPFESLWADLVQKIPPPPNVAGPDDIRNF 382
DB 247 DLLVKLFVREPEKRLVGRGD--LRQHPLEINWELEKEIDPPPRPKVSPFFDCSNF 303

QY 383 DTAFTETVYSCVSDSYDINVASVLEADDAFVGFSYAPP 423
DB 304 DKEFLNEKPLSLF---ADRALINSM---DQNMFRNFSFMNP 338

RESULT 11
US-11-132-142-7
; Sequence 7, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Saccharomyces sp.
US-11-132-142-7

Query Match      29.0%; Score 657.5; DB 7; Length 398;
Best Local Similarity 41.6%; Pred. No. 2.4e-51;
Matches 127; Conservative 64; Mismatches 107; Indels 7; Gaps 5;

QY 93 TDFDLKVIKGSFGKVLAKKLDGKFAVAVKVLQKIVLNKKEQKHMAERNVLLKNVK 152
DB 86 SDFQILRTLTGTSFGVRLIRSNHNGRFYALKTKKHITVKKQVEHNDERR-MUSIVS 144

QY 153 HPFLVGLHYSFQTEKLYFVLDFVNGGELFFHLQERSFPEHRAFYAAIASALGYLHS 212
DB 145 HPPIRMWGTQDSQQQFWMDYIEGELFSLLRKSKQRFNPNVAKFYAAEVCLEVLHS 204

QY 213 IKIVYRDLKPNILLDSVGHVLTDFGLCKEGIAISDTTTCGTPPEYLAPVIRKOPYD 272
DB 205 KDIIYRDLKPNILLDKNGHKIKITDFGFAK---YVPDVTVTLCGTPDYIAPEVVSTKPYN 261
```

QY 273 NTVDWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLRPGVSLTAWSIILEELKDX 332
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 262 KSDVMSFGVLIYEMLAGYTPFNSNTMKTYENILNAELKFPFPFHPDQDLKKUITRD 321
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 333 QNRNLGAKEDFLE-IQNHPFESLSWADLVQKKIPFPNPNV-AGPDDIRNFDTAFTET 390
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 322 LSRNLGNLQNGSDVKNHPWFNEVIEKLLARIYETPEPPIQGGQDTSQFD-RYPEEE 380
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :

QY 391 VPYSV 395

Db 381 FNYGI 385

RESULT 12

US-11-092-168-4
; Sequence 4, Application US/11092168
; Publication No. US2005027658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, HaiYong
; APPLICANT: Bears, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-092-168-4

Query Match 28.8%; Score 654.5; DB 7; Length 341;
Best Local Similarity 41.9%; Pred. No. 3.6e-51;
Matches 131; Conservative 55; Mismatches 120; Indels 7; Gaps 5;

QY 84 PSGNPHAKPTDPPFLKVIKGSFGKVLAKRKLDGKFYAVKVLQKKIVLNKKEQKHIMAE 143
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 24 PSQNT-AQLDQDFRIKTLGTSGFGRVMLVKHESGNHYAMKILDQKVKLQKIEHTLNE 82
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 144 RNVLNKNVHPFLVGLHYSQTTEKLYFVLDFVNGGELPFLHLOERSFPEHRARFYAAEI 203
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 83 KRI-LQAVNPFPLVLUKEFSKNSNLYMVMYVAGGEMFSLRRIGRFAEPHARFYAAQI 141
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 204 ASALGYLHSTIKIVYRDLKPNILLDSVGHVLTDFGLCKEGIAISDTTTCGTPEYLAP 263
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 142 VLTFEYLHSLDLIYRDLKPNILLDQGGYIQVTDGFAKR---VGRTWTLCTGTPYLAP 198
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 264 EVTRKQPDYNTVDWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLRPGVSLTAW 323
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 199 EILSKGYNKAVDWALGVLIYEMAAGYPPFADQPIQIYEKIVSGKVRFPFSSHSDLDK 258
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 324 ILEELLEKQRNLG-AKEDFLEIQNHPPFESLSWADLVQKKIPFPNPNVAGPDDIRNF 382
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :

Db 259 LLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATTDWIAIYQRKVEAPFIPKFGPGDTSNF 318
QY 383 DTAFTETVPYSV 395
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 319 DD-YEEEEIRVSI 330
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
RESULT 13
US-11-132-142-13
; Sequence 13, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-11-132-142-13

Query Match 28.6%; Score 650; DB 7; Length 351;
Best Local Similarity 41.9%; Pred. No. 9.6e-51;
Matches 127; Conservative 56; Mismatches 114; Indels 6; Gaps 4;

QY 94 DFDLKVIGKSGFGKVLAKRKLDGKFYAVKVLQKKIVLNKKEQKHIMAEARNVLLKNVKH 153
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 43 DFDKMTLGTSGFGRVMLVKHGAQYYAMKILDQKVKLQKIEHTLNEKRI-LQAVNF 101
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 154 PFLVGLHYSFOTTEKLYFVLDFVNGGELPFFHLOERSFPEHRARFYAAIASALGYLH 213
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 102 PELVRLEYSFKNSNLYMIMEYVPGGEMFSLRRIGRFAEPHARFYAAQIVLTTFEYLH 161
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 214 KIVYRDLKPNILLDSVGHVLTDFGLCKEGIAISDTTTCGTPEYLAPVIRKQPDY 273
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 162 DBIYRDLKPNILLDQGGYIQVTDGFAKR---VGRTWTLCTGTPEYLAPVIRKQPDY 218
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 274 TVDWMCLGAVLYEMLYGLPPFYCRDVAEMYNILHKPLSLRPGVSLTAWSIILEELK 333
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 219 AVDMWALGVLIYEMAAGYPPFADQPIQIYEKIVSGKVRFPFSSHSDLDKLLRNLLQ 278
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 334 QNRNLG-AKEDFLEIQNHPPFESLSWADLVQKKIPFPNPNVAGPDDIRNFDTAFTET 392
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 279 TKRYGNLKNVNDIKNHKWFATTDWIAIYQRKVEAPFIPKCRGPGDTSNFD-EEEDIR 337
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
QY 393 YSV 395
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
Db 338 VSL 340
:||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :
RESULT 14
US-11-132-142-9
; Sequence 9, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698

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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:12:00 ; Search time 12.6811 Seconds
(without alignments)
3254.993 Million cell updates/sec

Title: US-09-868-131A-4
Perfect score: 2269
Sequence: 1 MALKIPAKRIFGDNFDPDFI.....EADDAVFVGSYAPPSDLFL 429

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1475	65.1	431	2 A48094	serum and glucocor
2	1019.5	44.9	422	2 T26334	hypothetical prote
3	870	38.3	462	1 T17287	protein kinase (EC
4	866.5	38.2	479	1 A59380	protein kinase (EC
5	860.5	37.9	454	1 JC4345	protein kinase (EC
6	850.5	37.5	611	1 A55888	protein kinase (EC
7	844.5	37.2	481	1 A46288	protein kinase (EC
8	839	37.0	479	2 A38578	protein kinase 2 (
9	834.5	36.8	481	1 JC2438	protein kinase (EC
10	820.5	36.2	480	1 JC2437	protein kinase (EC
11	818.5	36.1	480	1 S33364	protein kinase (EC
12	818.5	36.1	763	1 A40831	gag-akt polyprotei
13	816.5	36.0	480	1 A39360	protein kinase (EC
14	810	35.7	586	2 A53758	protein kinase (EC
15	804.5	35.5	480	1 S62117	protein kinase (EC
16	804	35.4	680	2 S37955	protein kinase ypk
17	803.5	35.4	587	2 A49509	protein kinase C (
18	800	35.3	677	2 JS0178	protein kinase YKR
19	795.5	35.1	569	2 T50414	probable prolifera
20	790.5	34.8	737	1 KIMSCE	protein kinase C (
21	790	34.8	634	1 B32392	protein kinase C (
22	789	34.8	525	1 A41687	ribosomal protein
23	789	34.8	525	1 S12906	probable ribosomal
24	786.5	34.7	481	2 JE0377	p70 S6 kinase (EC
25	785	34.6	736	1 KIRBCE	protein kinase C (
26	780	34.4	525	1 TVRTK6	ribosomal protein
27	779.5	34.4	737	1 S28942	protein kinase C (
28	777	34.2	547	2 T22856	hypothetical prote
29	774	34.1	707	1 A53530	protein kinase C (

30	773.5	34.1	737	1 KIRTCE	protein kinase C (
31	764	33.7	696	2 S55694	protein kinase (EC
32	763	33.6	672	1 KIHUCA	protein kinase C (
33	763	33.6	672	1 KIMSCA	protein kinase C (
34	762	33.6	672	1 KIRBC	protein kinase C (
35	761	33.5	672	1 KIRTC	protein kinase C (
36	760.5	33.5	546	1 T43233	protein kinase (EC
37	760	33.5	672	1 KIBOC	protein kinase C (
38	757	33.4	646	2 T38171	probable serine/th
39	753	33.2	541	1 T43232	protein kinase (EC
40	753	33.2	592	2 JN0877	protein kinase C (
41	751	33.1	592	1 A30314	protein kinase C (
42	751	33.1	592	1 JC1480	protein kinase C (
43	750.5	33.1	528	1 T21523	protein kinase (EC
44	740.5	32.6	483	1 T43234	protein kinase (EC
45	740	32.6	683	1 A23690	protein kinase (EC

ALIGNMENTS

RESULT 1

A48094
serum and glucocorticoid-regulated kinase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A48094
R;Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.
Mol. Cell. Biol. 13, 2031-2040, 1993
A;Title: Characterization of sgk, a novel member of the serine/threonine protein kinase
A;Reference number: A48094; MUID:93204949; PMID:8455596
A;Accession: A48094
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-431 <WEB>
A;Cross-references: UNIPARC:UPI000017A3B8
A;Experimental source: Con8.hdc mammary epithelial tumor cells
A;Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBIP:127619)
C;Keywords: ATP
F;96-355/Domain: protein kinase homology <KIN>
F;104-112/Region: protein kinase ATP-binding motif

Query Match	65.1%	Score	1476;	DB 2;	Length	431;
Best Local Similarity	67.7%	Pred. No.	6.2e-63;			
Matches	281;	Conservative	50;	Mismatches	70;	Indels 14; Gaps 3;
Qy	19	FIKQRRAGLNEFTQNLVRYPDELNHPDRAFLQMDSPKH-----QSDPSEDEDEKSSQKLH	74			
Db	27	FMKQRRMGLNDFIQKLANNSSACKHPEVQSYLKISQFQPELMNANSPPPP-----	77			
Qy	75	STSQNLNPGSGNPHAKPTDFDKLVIGKSGFGKLLAKRKLQKGFYAVKVLQKIVLNR	134			
Db	78	SPSQQLNPGSSNPHAKPSDFHFLKVIKSGFGKLLARHKAEEAFYAVKVLQKALKKK	137			
Qy	135	KEQKHMAERNVLLKNVGHFVLGLHYSFQTTKLYFVLDFVNGGELFFHQLQERSFPFH	194			
Db	138	KEEKHIMSERVLLKNVGHFVLGLHFSFQTKLYFVLDFVNGGELFFHQLQERCLEP	197			
Qy	195	RARFYAAETASALGYLHSIKIVYRDILKPNILDSVGHVVLDTFGLCKEGIAISDTTTF	254			
Db	198	RARFYAAETASALGYLHSILNIVYRDILKPNILDSVGHVVLDTFGLCKENIEHNGTTSTF	257			
Qy	255	CGTPEYLAPVIRKQYDNTVDWMLGAVLYEMLYGLPPFYCYDVAEMYNILHKLPLSLR	314			
Db	258	CGTPEYLAPVIRKQYDRTVDWMLGAVLYEMLYGLPPFYSRNTAEYMNILNKPQLK	317			
Qy	315	PGVSLTAWSLIEELLEKDRNLCAKEDFLEIQNHFFESLSWADLVQKKIPPPFNVA	374			
Db	318	PNITNSARHLEGLLQKQRTKRLGAKDDFMEIKSHIFFSLINWDDLINKKITPPFNVS	377			
Qy	375	GPDDIRNFDPTAFTETVPYSCVSSYISVNASVLEADDAFVGFSYAPPSDPL	429			
Db	378	GPSDLRHDFEFTPEEPVSSIGRSPDSILVTASVKEAAEAFLGFSYAPPW-DSFL	431			

A;Residues: 1-479 <MAS>
A;Cross-references: UNIPARC:UPI00000335E8; GB:CAB53537; NID:G5804886; PIDN:CAB53537.1
C;Genetics:
A;Gene: GDB:AKT3; PKBG: PRKBG; RAC-gamma
A;Cross-references: GDB:9954867
A;Map position: 1q44-1q44
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;7-108/Domain: pleckstrin repeat homology <PK>
F;149-408/Domain: protein kinase homology <KIN>
F;157-165/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted
F;305/Binding site: phosphate (Thr) (covalent) #status predicted
F;474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 38.2%; Score 866.5; DB 1; Length 479;
Best Local Similarity 43.7%; Pred. No. 3.3e-34;
Matches 184; Conservative 65; Mismatches 145; Indels 27; Gaps 7;

QY 20 IKORRAGLNFQNLVRYPELVNHPDVRAFLQMDSPKHQSDPSZ-----DDED 68
Db 62 MKTERPKNTFIIRCLQWTV-----IERTFHVDTPEEREWEITAQVADRLQORQEEER 116
QY 69 SSQKLHSTSONINLG-----PSGNPHAKPT--DFDLKVIKSGFGKVLAKRKLQDGKFY 121
Db 117 --MNCSPTSQIDNIGSEEMDASTTHHKRKTWDFYLLKLGKGTGFKVILVREKASGKY 174
QY 122 AVKVLQKKIVLNKKEQKHMAERNVLLKNVHPPLVGLHYSFQTTEKLYFVLDVFNNGEL 181
Db 175 AMKILKKEVIIAKDEVAHTLTESRV-LKNTRHPPLTSLKYSFQTKDRLCFVMEVYNGEL 233
QY 182 FFHLQRRSPPEHRARYFAAEIASALGYLSIKIVYRDLPENILLSVGHVLTDFGLC 241
Db 234 FFHLRSRVFSEDRTRFYGAIEVSALDYLSHGKIVYRDLPENILLSVGHVLTDFGLC 293
QY 242 KEGIAISDTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFCRDVAE 301
Db 294 KEGITDAATWKTTCGTPPEYLAPEVLENDYGRAVDMWGLGVVMEYMGRLPFYVNDQHEK 353
QY 302 MYDNILHKPLSLRPGVSLTAWSLLELEKDRQNL--GAKEDFLEIQNHPPFESLSWADL 360
Db 354 LFELILMEDIKFPRTLSSDAKSLGILLIKDPNKRLLGGPDPAKEIMRHSFFSGVNNQDV 413
QY 361 VQKIPPPFPNPVAGPDIDRNFDTAFTTEETVPYSVCVSSYIVNASVLEADAFVGFYSY 420
Db 414 YDKKLVPFPKQVTSSETDTRYFDEEFTAQTITITPPEKYDEGDMCDNERRPHFPQFSY 473
QY 421 A 421
Db 474 S 474

RESULT 5
JC4345
protein kinase (EC 2.7.1.37) akt3 [validated] - rat
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C;Accession: JC4345
R;Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K
Biochem. Biophys. Res. Commun. 216, 526-534, 1995
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase
e C subtypes and beta gamma subunits of G proteins.
A;Reference number: JC4345; MUID:96063640; PMID:7488143
A;Accession: JC4345
A;Molecule type: mRNA
A;Residues: 1-454 <KON>
A;Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DBJ:D49836; NID:g1136777; PT
A;Experimental source: brain
C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
F;4-105/Domain: pleckstrin repeat homology <PLK>
F;146-405/Domain: protein kinase homology <KIN>
F;154-162/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted

Query Match 37.9%; Score 860.5; DB 1; Length 454;
Best Local Similarity 45.5%; Pred. No. 5.9e-34;
Matches 178; Conservative 61; Mismatches 125; Indels 27; Gaps 7;

QY 20 IKORRAGLNFQNLVRYPELVNHPDVRAFLQMDSPKHQSDPSZ-----DDED 68
Db 62 MKTERPKNTFIIRCLQWTV-----IERTFHVDTPEEREWEITAQVADRLQORQEEER 116
QY 69 SSQKLHSTSONINLG-----PSGNPHAKPT--DFDLKVIKSGFGKVLAKRKLQDGKFY 121
Db 117 --MNCSPTSQIDNIGSEEMDASTTHHKRKTWDFYLLKLGKGTGFKVILVREKASGKY 174
QY 122 AVKVLQKKIVLNKKEQKHMAERNVLLKNVHPPLVGLHYSFQTTEKLYFVLDVFNNGEL 181
Db 175 AMKILKKEVIIAKDEVAHTLTESRV-LKNTRHPPLTSLKYSFQTKDRLCFVMEVYNGEL 233
QY 182 FFHLQRRSPPEHRARYFAAEIASALGYLSIKIVYRDLPENILLSVGHVLTDFGLC 241
Db 234 FFHLRSRVFSEDRTRFYGAIEVSALDYLSHGKIVYRDLPENILLSVGHVLTDFGLC 293
QY 242 KEGIAISDTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFCRDVAE 301
Db 294 KEGITDAATWKTTCGTPPEYLAPEVLENDYGRAVDMWGLGVVMEYMGRLPFYVNDQHEK 353
QY 302 MYDNILHKPLSLRPGVSLTAWSLLELEKDRQNL--GAKEDFLEIQNHPPFESLSWADL 360
Db 354 LFELILMEDIKFPRTLSSDAKSLGILLIKDPNKRLLGGPDPAKEIMRHSFFSGVNNQDV 413
QY 361 VQKIPPPFPNPVAGPDIDRNFDTAFTTEETVPYSVCVSSYIVNASVLEADAFVGFYSY 391
Db 414 YDKKLVPFPKQVTSSETDTRYFDEEFTAQTITITPPEKYDEGDMCDNERRPHFPQFSY 444

RESULT 6
A55888
protein kinase (EC 2.7.1.37) akt [similarity] - fruit fly (Drosophila melanogaster)
N;Alternate names: protein kinase B; RAC-PK; serine/threonine-specific protein kinase R
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A55888
R;Andjelkovic, M.; Jones, P.F.; Grosniklaus, U.; Cron, P.; Schier, A.F.; Dick, M.; Bil
J. Biol. Chem. 270, 4066-4075, 1995
A;Title: Developmental regulation of expression and activity of multiple forms of the D
A;Reference number: A55888; MUID:95181376; PMID:7876156
A;Accession: A55888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-611 <AND>
A;Cross-references: UNIPROT:Q24469; UNIPARC:UPI00000866BE; GB:X83510
C;Genetics:
A;Gene: FlyBase:RacPK
A;Cross-references: FlyBase:FBgn0013324
A;Start codon: ACG
A;Introns: 261/3; 327/3; 457/3; 535/3; 584/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon
F;105-209/Domain: pleckstrin repeat homology <PLK>
F;264-523/Domain: protein kinase homology <KIN>
F;272-280/Region: protein kinase ATP-binding motif
F;295/Active site: Lys #status predicted
F;423/Binding site: phosphate (Thr) (covalent) #status predicted

F:596/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted	
Query Match	37.5%; Score 850.5; DB 1; Length 611;
Best Local Similarity	49.9%; Pred. No. 2.3e-33;
Matches	172; Conservative 47; Mismatches 115; Indels 11; Gaps 4;
QY	54 SPKHQSDPSE-----DEDESSQKLHSTSONINLGPSSGNPHAKPTDFDFLKVIGKSGSFG 107
DB	222 TPSEQDTMDTDMWATIAEDLSQ---FSVOGTTCSNSSGVKKVTLENFELKVLGKGTG 278
QY	108 KVLAKRKLDGKFYAVKVLQKTIVLNRKEQKHMAERNVLLKNVKGPFLVGLHYSTQTTE 167
DB	279 KVLCREKATAKYAIKILKEVLIQDEVAHTLTESRV-LKSTNHPFLISLKYSTQND 337
QY	168 KLYFVLDFVNGGELFFHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPNELL 227
DB	338 RLCFVMQYVNGGELFWHLSHERIFTEORTFYGAEIISALGYLHSQGIIVYRDLKLENLL 397
QY	228 DSVGHVVLDFGLCKEGIAISDTTTCFCTPEYLAPEVIRKQPYDNTDWMCLGAVLYEM 287
DB	398 DKDGHKIVADFGLCKEDITYGRTTKTFCGTPPEYLAPEVLDDNDYGOAVDMWGTGVMYEM 457
QY	288 LYLGPFPYCRDVAEMYDNILHKPLSLRPGVSLTAWGILBELLEKDRQNR-L-GAKEDFLEI 346
DB	458 ICGRLFPYNRDHDVLFLLVVEVKFPNRNITDEAKNLLACLLAKDKPKRLGGGKDDVKEI 517
QY	347 QNHPPFESWADLVQKKIPLPPPNVAGPDDIRNFDTAFTETV 391
DB	518 QAHPFFASINWTDLVLKIPPPKPVQVSTDTRYDFKFTGTSV 562
RESULT 7	
A46288	
N;protein kinase (EC 2.7.1.37) akt2 - human	
C;Species: Homo sapiens (man)	
C;Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004	
C;Accession: A46288	
R;Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; T	
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992	
A;Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/th	
A;Reference number: A46288; MUID:93028445; PMID:1409633	
A;Accession: A46288	
A;Molecule type: mRNA	
A;Residues: 1-481 <CHE>	
A;Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M95936; NID:gl78325; PIDN:	
A;Note: sequence extracted from NCBI backbone (NCBIP:115859)	
C;Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.	
C;Genetics:	
A;Gene: GDB:AKT2	
A;Map position: 19q13.2-19q13.2	
C;Function:	
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin	
A;Pathway: signal transduction pathways regulating various processes	
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein	
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k	
F:4-106/Domain: pleckstrin repeat homology <PLK>	
F:150-409/Domain: protein kinase homology <KIN>	
F:158-166/Region: protein kinase ATP-binding motif	
F:181/Active site: Lys #status predicted	
Query Match	37.2%; Score 844.5; DB 1; Length 481;
Best Local Similarity	42.3%; Pred. No. 3.5e-33;
Matches	181; Conservative 76; Mismatches 148; Indels 23; Gaps 9;
QY	13 DNF---DPDFIKORAGLNEFIQNLVRYPEL-----YNHPD-----VRAFLQWDSFKQ 58
DB	53 NNFSVAECQLMKTERPRNPNTFVIRCIQWTVTIRTFHVDSPDREBWMRAIQWVNSLKQ 112
QY	59 SDPSED--EDERSQKLHSTSONINLGPSSGNPHAKPT--DFDFLKVIGKSGFKVLLAKR 114
DB	113 RAPGEDPMDYKCGSPSDSSSTTEMEVAVS-KARAKVTMNDFDYLLKLGKGTFFOKVLVRE 171

QY	115 KLDGKFYAVKVLQKKIIVLNKRKEQKHMAERNVLLKNVKHPFLVGLHYSTQTTEKLYFVLD 174
DB	172 KATGRYYAMKIIRKEVITAKDEVAHTVTESRV-LQNRHPFLTALKYAFQTHDRLCFVME 230
QY	175 FVNGGELFFHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPNELLDSVGHVV 234
DB	231 YANGGELFFHLGRERVFTTEARFYGAEIVSALEYLHSDVDVYRDIKLENMLDKDGHK 290
QY	235 LTDFGLCKEGIAISDTTTCFCTPEYLAPEVIRKQPYDNTDWMCLGAVLYEMLYGLPPF 294
DB	291 ITDFGLCKEGISDGAETMTKTCFCTPEYLAPEVLDDNDYGRAVDWGLGVVYEMMCGRLPF 350
QY	295 YCRDVAEMYDNILHKPLSLRPGVSLTAWGILBELLEKDRQNR-L-GAKEDFLEIQNHPPFE 353
DB	351 YNQDHERLFFELIMEEIRFPRTLSPKASLLAGLKKDKPKQRLGGGSPDAKEYMEHRFFL 410
QY	354 SLSWADLVQKKIPLPPPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADD 413
DB	411 SINQDVVQKKULPPPKPVQVSTVDTRYEDDEFTAQSI--TITPPDRYDSLGLELDQRT 468
QY	414 AFGFYSYA 421
DB	469 HFPQFSYS 476
RESULT 8	
A38578	
N;protein kinase 2 (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)	
C;Species: Dictyostelium discoideum	
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 31-Dec-2004	
C;Accession: A38578	
R;Haribabu, B.; Dottin, R.P.	
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991	
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideu	
A;Reference number: A38578; MUID:91142122; PMID:1996312	
A;Accession: A38578	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-479 <CHAR>	
A;Cross-references: UNIPROT:P28178; UNIPARC:UPI0000131B58; GB:M59744; NID:gl67717; PIDN:	
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon.	
F:151-407/Domain: protein kinase homology <KIN>	
F:159-167/Region: protein kinase ATP-binding motif	
Query Match	37.0%; Score 839; DB 2; Length 479;
Best Local Similarity	47.1%; Pred. No. 6.4e-33;
Matches	177; Conservative 57; Mismatches 118; Indels 24; Gaps 7;
QY	53 DSPKQSDPSEDEDESSQKLHSTSONINLGPSSGNPHAKPTDFDFLKVIGKSGFKVLLA 112
DB	120 DSPNGSGNGNDDDEGPEVIFSKNQ-----SATKDDFELLNVIGKSGFKVMQV 170
QY	113 KEKLDGKFYAVKVLQKKIIVLNKRKEQKHMAERNVLLKNVKHPFLVGLHYSTQTTEKLYFV 172
DB	171 KKKGDKKIPAMVKLRDAIIARKQVNHKSEKII-LQCISHFPIVNLHVAFTQDKLYMV 229
QY	173 LDFVNGGELFFHLQERSFPFHRARFYAAEIASALGYLHSIKIVYRDLKPNELLDSVGH 232
DB	230 LDFVNGGELFFHLKREGREFPRVKIYAAEIVSALDHLHKQDIVYRDLKPNELLDSGEH 289
QY	233 VVLTFGLCKEGIAISDTTTCFCTPEYLAPEVIRKQPYDNTDWMCLGAVLYEMLYGLP 292
DB	290 ICITDFGLSKK-IETTDGTFCTGTPPEYLAPEVLNGHGHGCAVDMWMSLTLLYEMLTGTP 348
QY	293 PFCVDRDVAEMYDNILHKPLSLRPGVSLTAWGILBELLEKDRQNR-LGAKEDFLEIQNHPPF 352
DB	349 PFCVQVSTVWYQKILNGELKIPITYISPEAKSLLEGLLTREVDRKLTGTTGGG-EVKQHPWF 407
QY	353 ESLSWADLVQKKIPLPPPNVAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLY--- 409
DB	408 KNIDWEKLDKREVEVHFVKPKVSGTDSIQIDPVFTQER-PMD-----SLVETSALGDA 459

A;Molecule type: mRNA
A;Residues: 1-480 <BEL>
A;Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PID
C;Genetics:
A;Gene: MGI:87986
A;Cross-references: MGI:87986
A;Map position: 12
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes
A;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match 36.1%; Score 818.5; DB 1; Length 480;
Best Local Similarity 40.8%; Pred. No. 5.9e-32;
Matches 183; Conservative 63; Mismatches 145; Indels 57; Gaps 11;

QY 17 PDFIKORRAGLNEFIQNLVRYPELY--NHPDVRAFL-----QMDSPKHQSDPSEDED 66
DB 42 PQVDQRESPLNNF---SVAQCQLMKTERPRNPTFIIRCLQWTTVIERTFHVETPEEREE 98
QY 67 -----ERSSQKLHSTQINILGPS-----GNPHAKPT--DFDFLKVIGK 103
DB 99 WATAIQTVADGLKROBEETMDPRSGSPSDNSGAEMEVSIAKPKHRVTWNEFEYLKLGK 158
QY 104 GSGFGVLLAKRLDQGFYAVKVLQKIVLNLRKEQKHMAERNVLLKNVHPFLVGLHYSF 163
DB 159 GTFGKVLVKEKATGRYYAMKILKEVIVAKDEVAHTLTE--NRVLQNSRHPFLTALKYSF 217
QY 164 QTTEKLYFVLDPVNGGELFFHLQRRSFPEHRAFYAAETASALGYLHSLK-IVYRDLKP 222
DB 218 QTHRLCFVMEYANGGELFFHLRSRPFSEDRARFYGAIEVSALDYLSHSEKNVYRDLKL 277
QY 223 ENILDSVGHVLTDFGLCKEGIAISDTTTFCTGTPYLAPEVIRKQPDNTVDWMCGLG 282
DB 278 ENLMLDKOGHIKITDFGLCKEGIKDGAATWKTFCTGTPYLAPEVLENDYGRAVDWMLGLV 337
QY 283 VLYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNL-CAKE 341
DB 338 VMYEMMCGRLPFYFNQDHEKLFELILMEIRFPRTLGPPEAKSLLSGLLKXDPQRLGGSGE 397
QY 342 DFLEIQNHPPFESLSWADLVQKKIPPPENPNVAGPDDIRNFDTAFTTEETVPYS----- 394
DB 398 DAKIEMQHRFFANIVMQDVYEKLSPPFPQVTSSETDTRYFDEEFTAQMITITPPDQDSDS 457
QY 395 -VCVSSDYSIVNASVLEADDAFVGFSYA 421
DB 458 MECVDS-----ERRPHFPQFSYS 475

RESULT 12
A40831
gag-akt polypeptide - AKT8 murine leukemia virus
N;Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin
C;Species: AKT8 murine leukemia virus
C;Date: 12-Feb-1993 #sequence_revision 12-May-1994 #text_change 31-Dec-2004
C;Accession: A40831; B40831
R;Bellacosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.
Science 254, 274-277, 1991
A;Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH
A;Reference number: A40831; MUID:92022574; PMID:1833819
A;Accession: A40831
A;Molecule type: DNA
A;Residues: 1-262 <BEL>
A;Cross-references: UNIPARC:UPI00001725AF; GB:M80675
A;Accession: B40831
A;Molecule type: DNA

A;Residues: 262-763 <BE2>
A;Cross-references: UNIPARC:UPI00001725B0; GB:M80675
C;Genetics:
A;Gene: gag-akt
C;Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransfera
F;1-129/Product: core protein p15 #status predicted <CP1>
F;130-214/Product: inner coat protein p12 #status predicted <CP2>
F;284-763/Domain: kinase-related transforming protein akt #status predicted <AKT>
F;287-389/Domain: pleckstrin repeat homology <PLK>
F;431-691/Domain: protein kinase homology <KIN>
F;439-447/Region: protein kinase ATP-binding motif
F;25-337/Binding site: carboxylate (Asn) (covalent) #status predicted
F;462/Active site: Lys #status predicted
F;609/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 36.1%; Score 818.5; DB 1; Length 763;
Best Local Similarity 40.8%; Pred. No. 9.1e-32;
Matches 183; Conservative 63; Mismatches 145; Indels 57; Gaps 11;

QY 17 PDFIKORRAGLNEFIQNLVRYPELY--NHPDVRAFL-----QMDSPKHQSDPSEDED 66
DB 325 PQVDQRESPLNNF---SVAQCQLMKTERPRNPTFIIRCLQWTTVIERTFHVETPEEREE 381
QY 67 -----ERSSQKLHSTQINILGPS-----GNPHAKPT--DFDFLKVIGK 103
DB 382 WATAIQTVADGLKROBEETMDPRSGSPSDNSGAEMEVSIAKPKHRVTWNEFEYLKLGK 441
QY 104 GSGFGVLLAKRLDQGFYAVKVLQKIVLNLRKEQKHMAERNVLLKNVHPFLVGLHYSF 163
DB 442 GTFGKVLVKEKATGRYYAMKILKEVIVAKDEVAHTLTE--NRVLQNSRHPFLTALKYSF 500
QY 164 QTTEKLYFVLDPVNGGELFFHLQRRSFPEHRAFYAAETASALGYLHSLK-IVYRDLKP 222
DB 501 QTHRLCFVMEYANGGELFFHLRSRPFSEDRARFYGAIEVSALDYLSHSEKNVYRDLKL 560
QY 223 ENILDSVGHVLTDFGLCKEGIAISDTTTFCTGTPYLAPEVIRKQPDNTVDWMCGLG 282
DB 561 ENLMLDKOGHIKITDFGLCKEGIKDGAATWKTFCTGTPYLAPEVLENDYGRAVDWMLGLV 620
QY 283 VLYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSIIEELLEKDRQNL-CAKE 341
DB 621 VMYEMMCGRLPFYFNQDHEKLFELILMEIRFPRTLGPPEAKSLLSGLLKXDPQRLGGSGE 680
QY 342 DFLEIQNHPPFESLSWADLVQKKIPPPENPNVAGPDDIRNFDTAFTTEETVPYS----- 394
DB 681 DAKIEMQHRFFANIVMQDVYEKLSPPFPQVTSSETDTRYFDEEFTAQMITITPPDQDSDS 740
QY 395 -VCVSSDYSIVNASVLEADDAFVGFSYA 421
DB 741 MECVDS-----ERRPHFPQFSYS 758

RESULT 13
A59360
protein kinase (EC 2.7.1.37) akt1 [validated] - human
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
C;Accession: A39360; S36389; S18000; S20836
R;Jones, P.F.; Jakubowicz, T.; Pitosasi, F.J.; Maurer, F.; Hemmings, B.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991
A;Title: Molecular cloning and identification of a serine/threonine protein kinase of t
A;Reference number: A39360; MUID:91239529; PMID:1851997
A;Accession: A39360
A;Molecule type: mRNA
A;Residues: 1-480 <JON>
A;Cross-references: UNIPROT:P31749; UNIPARC:UPI000002E75B; GB:M63167; NID:g190827; PID
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A;Reference number: S24423; MUID:92249329; PMID:1533586
A;Accession: S36389
A;Status: nucleic acid sequence not shown; translation not shown

S62117
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: S62117; S24423; S17999; S15714; S36388
R;Coffer, P.J.; Woodgett, J.R.
submitted to the EMBL Data Library, December 1991
A;Reference number: S62117
A;Accession: S62117
A;Molecule type: mRNA
A;Residues: 1-480 <COW>
A;Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:g630; PIDN:C
A;Note: this is a revision to the sequence from reference S17999
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A;Reference number: S24423; MUID:92249329; PMID:15333586
A;Contents: erratum
A;Accession: S24423
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 70-78,'N',80-145 <COW>
A;Cross-references: UNIPARC:UPI0001725AD; EMBL:X61036
A;Note: this is a revision to the sequence from reference S17999
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
A;Reference number: S17999; MUID:92037600; PMID:1718748
A;Accession: S17999
A;Molecule type: mRNA
A;Residues: 1-70,'TPSSAACSGPRSSARSTWRPRSGVDHRRHPCGRRRAQAGGGDGLPVGLTRRELGGRGVGAGOP
A;Cross-references: UNIPARC:UPI0001725AE; EMBL:X61036
A;Note: this sequence has been revised in references S62117 and S24423
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 35.5%; Score 804.5; DB 1; Length 480;
Best Local Similarity 39.9%; Pred. No. 2.7e-31;
Matches 180; Conservative 66; Mismatches 142; Indels 63; Gaps 11;
QY 17 PDFIKORRAGLNEFIQNLVRYPELY--NHPDVRAFL-----QMDSPKHQSDPSEDED 66
DB 42 PQDLEQRESPLNPF---SVAQCQLMKTERPRNPFTIIRCLQWTTVIERTFHVETPEERE 98
QY 67 -----ERSSQKLHSTSQINILGPS-----GNPHAKPT--DFDFLKVIGK 103
DB 99 WTTAIQTVDGLKXQREETWDFRSGPGSGNGAEVSLAKPKHRTWNEFEYVKLIGK 158
QY 104 GSEFGVLLAKRKLDGKFYAVKVLQKXIVLNKKEQKIMAEERNVLLKNVKHPFLVGLHYSF 163
DB 159 GTFGKVLVKEKATAAYYAMKILKEVIAKDEVAHTLT-E-NRVLQNSRHPSLTALKYSF 217
QY 164 QTTEKLYFVLDFVNGSELPFHLORESRFPFHRARFAAEIASALGYLHSIK-IVYRDLKP 222
DB 218 QTHRLCLFVMEYANGGELFFHLRSERVFSDRARFYGAIEVSALDYLSHSEKEYVYRDLKL 277
QY 223 ENILLDSVGHVLTDFGLCKEGIAISDTTTTCGTPEYLAPEVIRKOPYDNTVDWMCLGA 282
DB 278 ENMLDKDGHKITDFGLCKEGIKDGNATMKTFCGTPEYLAPEVLENDYGRAVDWMGLGV 337
QY 283 VLYEMLYGLPPFYCRDVAEMYDNIHLKPLSLRFGVSLTAWSIILEELLEKDRQNRL-CAKE 341
DB 338 VMYEMMCGRLPFYFNQDHEKLFELILMBEIRFPRTLSPEAKSLISGLLKKDPKQRLGGSE 397

QY 342 DFLEIQNHPPFESLSWADLVOKKIIPPFPNPVAGDDIRNFDATFTEETVPKSVCVSSDY 401
DB 398 DAKEMQHRFFASIVQDVYKLGSPFPKPQVTSETDTRFYDFDEEFTAQ----- 445
QY 402 SIVNASVLEADDAFVG-----FSYA 421
DB 446 -MITITPPDQDDSMEGVDSERRRPHFPQFSYS 475

Search completed: January 27, 2006, 23:32:05
Job time : 13.6811 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:08:15 ; Search time 69.8811 Seconds
(without alignments)
4331.236 Million cell updates/sec

Title: US-09-868-131A-4
Perfect score: 2269
Sequence: 1 MALKIPAKRIFGNFDPDFI.....EADDAFVGSYAPPSDLFL 429

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2269	100.0	429	1	Q6FHV7 HUMAN
2	2269	100.0	496	1	SGK3 HUMAN
3	2269	100.0	496	2	Q5R7A7 PONPY
4	2264	99.8	496	2	Q5H9Q5 HUMAN
5	2261	99.6	496	2	Q53EW6 HUMAN
6	2210	97.4	429	1	Q8VEK1 MOUSE
7	2210	97.4	496	1	SGK3 MOUSE
8	2140	94.3	490	2	Q5ZJQ4 CHICK
9	1783	78.6	518	2	Q4SFC2 TETNG
10	1501	66.2	526	2	Q5V6S5 HUMAN
11	1482.5	65.3	421	2	Q5TCN4 HUMAN
12	1480	65.2	519	2	Q6NS85 MOUSE
13	1476	65.1	431	2	Q5TCN3 HUMAN
14	1476	65.1	431	2	Q68G05 RAT
15	1476	65.1	445	2	Q5TCN2 HUMAN
16	1474	65.0	432	2	Q6ULI9 CHICK
17	1473	64.9	431	2	Q4R633 MACFA
18	1472	64.9	431	1	SGK1 HUMAN
19	1468	64.7	431	1	SGK1 RABIT
20	1463	64.5	431	1	SGK1 MOUSE
21	1460	64.3	418	2	Q5BK44 XENTR
22	1458.5	64.3	430	1	SGK1 RAT
23	1457	64.2	434	2	Q6GPN6 XENLA
24	1456	64.2	434	2	Q93524 XENLA
25	1453.5	64.1	433	2	Q7ZTW4 BRARE
26	1452	64.0	431	2	Q5Q0U5 FUNHE
27	1447	63.8	594	2	Q73927 SQUAC
28	1442	63.6	434	2	Q6GLY8 XENLA
29	1420.5	62.6	490	2	Q4RR91 TETNG
30	1414	62.3	433	2	Q73926 SQUAC
31	1328.5	58.6	427	1	SGK2 HUMAN

32	1328.5	58.6	427	2	Q5H8Y6 HUMAN	Q5H8Y6 homo sapien
33	1319.5	58.2	367	2	Q5RDZ9 PONPY	Q5rdz9 pongo pygma
34	1316.5	58.0	367	2	Q5TZR3 HUMAN	Q5tzr3 homo sapien
35	1313.5	57.9	393	2	Q52PK5 HUMAN	Q52pk5 homo sapien
36	1308	57.6	366	2	Q5H8Z1 HUMAN	Q5h8z1 homo sapien
37	1297.5	57.2	367	1	SGK2 MOUSE	Q9qz85 mus musculus
38	1292.5	57.0	350	2	Q4S7Y9 TETNG	Q4s7y9 tetraodon n
39	1241.5	54.7	1114	2	Q4SVX7 TETNG	Q4svx7 tetraodon n
40	1214	53.5	302	1	SGK2 RAT	Q8r4u9 rattus norv
41	1186.5	52.3	1550	2	Q4SY70 TETNG	Q4sy70 tetraodon n
42	1159	51.1	279	2	Q8R4V0 RAT	Q8r4v0 rattus norv
43	1110	48.9	285	2	Q5H8Y4 HUMAN	Q5h8y4 homo sapien
44	1039	45.8	316	2	Q4RI65 TETNG	Q4ri65 tetraodon n
45	1019.5	44.9	422	2	Q94365 CAEEL	Q94365 caenorhabdi

ALIGNMENTS

RESULT 1
Q6FHV7_HUMAN
ID Q6FHV7_HUMAN PRELIMINARY; PRT; 429 AA.
AC Q6FHV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE SGKL protein.
DE Name=SGKL;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mfoundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR536581; CAG38818.1; -, mRNA.
DR SMR; Q6FHV7; 1-58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001683; PX.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS0195; PX; 1.
SQ SEQUENCE 429 AA; 49004 MW; 2DD1F5ADD6C4234C CRC64;

Query Match 100.0%; Score 2269; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 9,9e-140;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALKIPAKRIFGNFDPDFIKQRRAGINEFIQNLVRYPELYNHPDVRAFIQLQMDSPKQSD 60
Db 1 MALKIPAKRIFGNFDPDFIKQRRAGINEFIQNLVRYPELYNHPDVRAFIQLQMDSPKQSD 60
Qy 61 PSEDEDSQKLHSTSQINILGPSGNPHAKPTDFDFLKVIGKSGFKVLAKRKLQDKF 120

Db 61 PSEDEDESSQKLHSTSQINILGSPGNPHAKPTDFDFLKVIGKSGFQVLLAKRKLQDKF 120
Qy 121 YAVKVLQKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 180
Db 121 YAVKVLQKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSQTTEKLYFVLDFVNGGE 180
Qy 181 LFFHLQERSFPPEHRAFYAAETASALGYLHSTIKIVVRDLKPNILLDSVGHVVLTDGFL 240
Db 181 LFFHLQERSFPPEHRAFYAAETASALGYLHSTIKIVVRDLKPNILLDSVGHVVLTDGFL 240
Qy 241 CKEGIAISDTTTFCCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
Db 241 CKEGIAISDTTTFCCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
Qy 301 EMDYDNLHKPLSLRPGVSLTAWSLBELLEKQNRILGAKEDFLEIQNHFFESLSWADL 360
Db 301 EMDYDNLHKPLSLRPGVSLTAWSLBELLEKQNRILGAKEDFLEIQNHFFESLSWADL 360
Qy 361 VQKKIPPPNPVAGPDDIRNFDTAFTTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Db 361 VQKKIPPPNPVAGPDDIRNFDTAFTTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
Qy 421 APPSEDLFL 429
Db 421 APPSEDLFL 429

RESULT 2

SGK3 HUMAN
ID SGK3 HUMAN STANDARD; PRT; 496 AA.
AC Q96BRL; Q9P1Q7; Q9UKG5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk3 (BC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 3) (Serum/glucocorticoid
DE regulated kinase-like).
DE Names=SGK3; Synonyms=SGK3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, PHOSPHORYLATION SITE THR-320, AND MUTAGENESIS OF
RP SER-486.
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021.3440189;
RX Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel,
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20054360; PubMed=10595774; DOI=10.1006/geno.1999.5969;
RX Dai F., Yu L., He H., Zhao Y., Yang J., Zhang X., Zhao S.;
RT "Cloning and mapping of a novel human Serum/Glucocorticoid regulated
RT kinase-like gene, SGK1, to chromosome 8q12.3-q13.1.";
RL Genomics 62:95-97(1999).
RN [3]
RP SEQUENCE REVISION.
RX Zhao Y.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Mammary gland;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=22284526; PubMed=12397388; DOI=10.1007/s00424-002-0873-2;
RX Gamber N., Fillon S., Feng Y., Friedrich B., Lang P.A., Henke G.,
RA Huber S.M., Kobayashi T., Cohen P., Lang F.;
RT "K(+) channel activation by all three isoforms of serum- and
RT glucocorticoid-dependent protein kinase SGK.";
RL Pflügers Arch. 445:60-66(2002).
CC -!- FUNCTION: Involved in the activation of potassium channels.
CC Mediates cell IL-3-dependent survival signals (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized in vesicle-like structures and in
CC the early endosome (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in most tissues with highest levels
CC in pancreas, kidney liver, heart and brain and lower levels in
CC lung, placenta and skeletal muscle.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Contains 1 PK (phox homology) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF169035; AAF12758.1; ALT INIT; mRNA.
DR EMBL; AF085233; AAF27051.2; -; mRNA.
DR EMBL; BC015326; AAH15326.1; -; mRNA.
DR HSSP; P31751; 1GZK.
DR SMR; Q96BRL; 10-125.
DR Ensembl; ENSG00000104205; Homo sapiens.
DR HGNC; HGNC:10812; SGK1.
DR MIM; 607591; -.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0006950; P:response to stress; TAS.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001683; PK.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; I.
DR Pfam; PF00433; Pkinase_C; 1.
DR Pfam; PF00787; PK; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00312; PK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50195; PK; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 12 124 PK.
FT DOMAIN 162 419 Protein kinase.
FT NP_BIND 168 176 ATP (By similarity).
FT MOTIF 195 205 Nuclear localization signal (By similarity).
FT

FT ACT_SITE 286 286 Proton acceptor (By similarity).
 FT BINDING 191 191 ATP (By similarity).
 FT MOD_RES 320 320 Phosphothreonine (by PDPK1).
 FT MUTAGEN 486 486 S->D: Increased activation.
 FT CONFLICT 54 54 F -> V (in Ref. 2 and 3).
 FT CONFLICT 127 127 D -> G (in Ref. 2 and 3).
 FT CONFLICT 187 187 F -> V (in Ref. 2 and 3).
 FT CONFLICT 294 294 L -> V (in Ref. 2 and 3).
 FT CONFLICT 387 387 T -> R (in Ref. 2 and 3).
 SQ SEQUENCE 496 AA; 57108 MW; 76A6CCEB69006CF1 CRC64;

Query Match 100.0%; Score 2269; DB 1; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.2e-139;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60
 DB 68 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 127

QY 61 PSEDEDRSSQKLHSTQNINLPGSGNPHAKPTDFDLKVGKSGFKVLLAKRKLQDKF 120
 DB 128 PSEDEDRSSQKLHSTQNINLPGSGNPHAKPTDFDLKVGKSGFKVLLAKRKLQDKF 187

QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
 DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 247

QY 181 LFPHLQRRSFPEHRARFYAAETASALGYLHSIKIVYRDLPENILDSVGHVVLDTDFGL 240
 DB 248 LFPHLQRRSFPEHRARFYAAETASALGYLHSIKIVYRDLPENILDSVGHVVLDTDFGL 307

QY 241 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
 DB 308 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVA 367

QY 301 EMYDNLHKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHFFFSLSWADL 360
 DB 368 EMYDNLHKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHFFFSLSWADL 427

QY 361 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
 DB 428 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487

QY 421 APPSEDLFL 429
 DB 488 APPSEDLFL 496

RESULT 3
 Q5R7A7_PONPY PRELIMINARY; PRT; 496 AA.
 AC Q5R7A7;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Hypothetical protein DKFZp469J0919.
 GN Name=DKFZp469J0919;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Pongo.
 NCBI_TaxID=9600;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RG The German cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amid C., Oanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; CR860211; CA92353.1; -, mRNA.
 DR SNR; Q5R7A7; 10-125.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Kinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001683; PX.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Kinase_I.
 DR Pfam; PF00433; Kinase_C; 1.
 DR Pfam; PF00787; PX; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00312; PX; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS0195; PX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 496 AA; 57108 MW; 76A6CCEB69006CF1 CRC64;

Query Match 100.0%; Score 2269; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.2e-139;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60
 DB 68 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 127

QY 61 PSEDEDRSSQKLHSTQNINLPGSGNPHAKPTDFDLKVGKSGFKVLLAKRKLQDKF 120
 DB 128 PSEDEDRSSQKLHSTQNINLPGSGNPHAKPTDFDLKVGKSGFKVLLAKRKLQDKF 187

QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
 DB 188 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 247

QY 181 LFPHLQRRSFPEHRARFYAAETASALGYLHSIKIVYRDLPENILDSVGHVVLDTDFGL 240
 DB 248 LFPHLQRRSFPEHRARFYAAETASALGYLHSIKIVYRDLPENILDSVGHVVLDTDFGL 307

QY 241 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVA 300
 DB 308 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVA 367

QY 301 EMYDNLHKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHFFFSLSWADL 360
 DB 368 EMYDNLHKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHFFFSLSWADL 427

QY 361 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
 DB 428 VQKKIPPPNPNVAGPDDIRNFDFTAFTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487

QY 421 APPSEDLFL 429
 DB 488 APPSEDLFL 496

RESULT 4
 Q5H9Q5_HUMAN PRELIMINARY; PRT; 496 AA.
 ID Q5H9Q5_HUMAN
 AC Q5H9Q5;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE Hypothetical protein DKFZp781N0293.
 GN Name=DKFZp781N0293;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;

OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG TISSUE=Colon carcinoma;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR933673; CAI45969.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50195; PX; 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 57094 MW; D4D5162DB3C4C447 CRC64;

Query Match 99.8%; Score 2264; DB 2; Length 496;
Best Local Similarity 99.8%; Pred. No. 2.5e-139;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
DB 68 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127
QY 61 PSEDEDESSQKLHSTSQNINLPGSGNPHAKPTDFDLKVIKSGSGKVLAKRKLDGKF 120
DB 128 PSEDEDESSQKLHSTSQNINLPGSGNPHAKPTDFDLKVIKSGSGKVLAKRKLDGKF 187
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180
DB 188 YAVNVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 247
QY 181 LPFHLQRRSFPHRRARFAAEATASALGVLSIKIVYRDLKPNILLDSVGHVLTDFGL 240
DB 248 LPFHLQRRSFPHRRARFAAEATASALGVLSIKIVYRDLKPNILLDSVGHVLTDFGL 307
QY 241 CKEGIAISDTTTFCTGTPYLAPEVIRKQPDYNTVDWCLGAVLYEMLGLPPFYCRDVA 300
DB 308 CKEGIAISDTTTFCTGTPYLAPEVIRKQPDYNTVDWCLGAVLYEMLGLPPFYCRDVA 367
QY 301 EMDYDNLHKLPLSLRPGVSLTAWSLLELLEKQRNLGAKEDFLEIQNHPPFRESLSWADL 360
DB 368 EMDYDNLHKLPLSLRPGVSLTAWSLLELLEKQRNLGAKEDFLEIQNHPPFRESLSWADL 427
QY 361 VQKKIPPPNPVAGPDDIRNFDTAFTTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 420
DB 428 VQKKIPPPNPVAGPDDIRNFDTAFTTEETVPYSCVSSDYSIVNASVLEADDAFVGFSY 487
QY 421 APPSEDLFL 429
DB 488 APPSEDLFL 496

RESULT 5

Q53EW6 HUMAN
ID Q53EW6_HUMAN PRELIMINARY; PRT; 496 AA.
AC Q53EW6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serum/glucocorticoid regulated kinase-like isoform 1 variant
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Maruyama K., Sugano S.;
RT "Oligo-capping : a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK223523; BAD97243.1; -; mRNA.
DR SWR; Q53EW6; 10-125.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001683; PX.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50195; PX; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ NON_TER 1
SQ SEQUENCE 496 AA; 57048 MW; 167C7EB74E9C47D0 CRC64;

Query Match 99.6%; Score 2261; DB 2; Length 496;
Best Local Similarity 99.8%; Pred. No. 3.9e-139;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 60
DB 68 MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSD 127
QY 61 PSEDEDESSQKLHSTSQNINLPGSGNPHAKPTDFDLKVIKSGSGKVLAKRKLDGKF 120
DB 128 PSEDEDESSQKLHSTSQNINLPGSGNPHAKPTDFDLKVIKSGSGKVLAKRKLDGKF 187
QY 121 YAVKVLQKKIVLNRKEQKHMAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDFVNGGE 180

Db 188 YAVKVLQKIVLNKEQKHMAERNVLLKNVHPPELVGLHYSFQTTEKLYFVLDVNGGE 247
Qy 181 LFFHLQERSPEPHRARFYAAEIASALGYLHSIKIVYRDLPENLLDSVGHVLTDFGL 240
Db 248 LFFHLQERSPEPHRARFYAAEIASALGYLHSIKIVYRDLPENLLDSVGHVLTDFGL 307
Qy 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
Db 308 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPPYCRDVA 367
Qy 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHPPFESLSWADL 360
Db 368 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHPPFESLSWADL 427
Qy 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 420
Db 428 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 487
Qy 421 APPSEDLFL 429
Db 488 APPSEDLFL 496

RESULT 6

Q8VEK1 MOUSE PRELIMINARY; PRT; 429 AA.
AC Q8VEK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sgk3 protein.
GN Name=Sgk3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=2238257; PubMed=12477937; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: BC018363; AAHL8363.1; -; mRNA.
DR HSSP: P31751; INRY.
DR SWR: Q8VEK1; 1-58.
DR MGI: 2182368; Sgk3.
GO: GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.

DR GO: GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO: GO:0006916; P:anti-apoptosis; IDA.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR001683; PX.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase_1.
DR Pfam: PF00433; Pkinase_C_1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00195; PX; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 429 AA; 49077 MW; A9C6B7A0C34031F3 CRC64;

Query Match 97.4%; Score 2210; DB 2; Length 429;
Best Local Similarity 97.0%; Pred. No. 6.9e-136;
Matches 416; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60
Db 1 MALKIPAKRIFGDNFDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKQSD 60
Qy 61 PSEDEDERSSQKLHSTSONINLPGSGNPHAKPTDFDLKVIKGSFGKVLAKRKLQKGF 120
Db 61 PSEDEDERSTSKPHSTSRNINLPGTGNPHAKPTDFDLKVIKGSFGKVLAKRKLQKGF 120
Qy 121 YAVKVLQKIVLNKEQKHMAERNVLLKNVHPPELVGLHYSFQTTEKLYFVLDVNGGE 180
Db 121 YAVKVLQKIVLNKEQKHMAERNVLLKNVHPPELVGLHYSFQTTEKLYFVLDVNGGE 180
Qy 181 LFFHLQERSFPEPHRARFYAAEIASALGYLHSIKIVYRDLPENLLDSVGHVLTDFGL 240
Db 181 LFFHLQERSFPEPHRARFYAAEIASALGYLHSIKIVYRDLPENLLDSVGHVLTDFGL 240
Qy 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
Db 241 CKEGIAISDTTTCGTPPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
Qy 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHPPFESLSWADL 360
Db 301 EMDYNIHLKPLSLRPGVSLTAWSLLELLEKDRQNLGAKEDFLEIQNHPPFESLSWADL 360
Qy 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 420
Db 361 VQKKIPPPFNPNVAGPDDIRNFDTAFTETVPYSVCVSSDYSIVNASVLEADDAFVGFSY 420
Qy 421 APPSEDLFL 429
Db 421 APPSEDLFL 429

RESULT 7

SGK3_MOUSE
ID SGK3_MOUSE STANDARD; PRT; 496 AA.
AC Q8VEK1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk3 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 3) (Serum/glucocorticoid
DE regulated kinase-like) (Cytokine independent survival kinase).
GN Name=Sgk1; Synonyms=Cisk, Sgk3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND MUTAGENESIS OF LYS-191.
RX MEDLINE=20504817; PubMed=11050396; DOI=10.1016/S0960-9822(00)00733-8;
RA Liu D., Yang X., Songyang Z.;
RT "Identification of CISK, a new member of the SGK kinase family that
RT promotes IL-3-dependent survival.";
RL Curr. Biol. 10:1233-1236(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RC STRAIN=C57BL/6J; TISSUE=Forelimb, Ovary, and Uterus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Shriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.D.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [3]
RP CHARACTERIZATION, AND MUTAGENESIS OF ARG-90.
RX MEDLINE=21405768; PubMed=11514587; DOI=10.1083/jcb.200105089;
RA Xu J., Liu D., Gill G., Songyang Z.;
RT "Regulation of cytokine-independent survival kinase (CISK) by the Phox
RT homology domain and phosphoinositides";
RL J. Cell Biol. 154:699-705(2001).
CC -I- FUNCTION: Involved in the activation of potassium channels (By
CC similarity). Mediates cell IL-3-dependent survival signals. Can
CC inhibit pro-apoptotic FOXO3a in vitro.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SUBCELLULAR LOCATION: Localized in vesicle-like structures and in
CC the early endosome.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9ERE3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9ERE3-2; Sequence=VSP_004934, VSP_004935;
CC Note=No experimental confirmation available;
CC -I- TISSUE SPECIFICITY: Widely expressed, predominantly in the heart,
CC spleen and 7-day embryo.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -I- SIMILARITY: Contains 1 PH (phox homology) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF312007; AAC34115.1; -, mRNA.
DR ENBL; AK028722; BAC26083.1; -, mRNA.

DR EMBL; AK030314; BAC26895.1; -, mRNA.
DR EMBL; AK031133; BAC27269.1; -, mRNA.
DR EMBL; AK031328; BAC27349.1; -, mRNA.
DR PDB; 1XTE; X-ray; A=7-160.
DR PDB; 1XTN; X-ray; A/B=7-126.
DR Ensembl; ENSMUSG0000025915; Mus musculus.
DR MGI; MGI:2182368; Sgk3.
DR GO; GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001693; PK.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR Pfam; PF00787; PK; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00312; PK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00195; PK; 1.
DR 3D-structure; Alternative splicing; ATP-binding; Kinase;
KW Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 12 124 PK.
FT DOMAIN 162 419 Protein kinase.
FT NP_BIND 168 176 ATP (By similarity).
FT MOTIF 195 205 Nuclear localization signal (By
FT similarity).
FT ACT_SITE 286 286 Proton acceptor (By similarity).
FT BINDING 191 191 ATP (By similarity).
FT MOD_RES 320 320 Phosphothreonine (by PDPK1) (By
FT similarity).
FT VARSPIC 327 333 YLAPEVI -> VRNMSDH (in isoform 2).
FT VARSPIC 334 496 Missing (in isoform 2).
FT MUTAGEN 90 90 R->A: Diminishes binding to
FT phosphoinositides.
FT MUTAGEN 191 191 K->A: No activity.
FT CONFLICT 114 114 R -> G (in Ref. 2; BAC27349).
FT CONFLICT 204 204 Q -> P (in Ref. 2; BAC27349).
SQ SEQUENCE 496 AA; 57145 MW; 4B7D2804A5948BAD CRC64;
Query Match 97.4%; Score 2210; DB 1; Length 496;
Best Local Similarity 97.0%; Pred. No. 8.2e-136;
Matches 416; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 MALKTPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQMDSPKHQSD 60
DB 68 MALKTPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQMDSPKHQSD 127
QY 61 PSEDEDESSQKLHSTSQNLINLPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLQDKF 120
DB 128 PSEDEDESRSTKPHSTSRNINLPGTGNPHAKPTDFDLKVIKGSFGKVLAKRKLQDKF 187
QY 121 YAVKVLQKKIVLNKREKQKHAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDVFNGGE 180
DB 188 YAVKVLQKKIVLNKREKQKHAERNVLLKNVHPFLVGLHYSFQTTEKLYFVLDVFNGGE 247
QY 181 LFFHQLQRRSFPEHRRARFYAAEIASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 240
DB 248 LFFHQLQRRSFPEHRRARFYAAEIASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGL 307
QY 241 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPYDNTVDWCLGAVLYEMLYGLPPFYCRDVA 300
DB 308 CKEGIAISDTTTFCTGTPPEYLAPEVIRKQPYDNTVDWCLGAVLYEMLYGLPPFYCRDVA 367

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QY 301 EMDNIIHKPLSLRPGVSLTAWSTLELLEKDRNRLGAKEDFLEIQNHPPFESLSWADL 360
Db 368 EMDNIIHKPLSLRPGVSLTAWSTLELLEKDRNRLGAKEDFLEIQNHPPFESLSWADL 427
QY 361 VQKIPPPNPVAGPDIDRNFDTAFTEETVPYVSVSSDYIVNASVLEADDAFVGFSY 420
Db 428 VQKIPPPNPVAGPDIDRNFDTAFTEETVPYVSVSSDYIVNASVLEADDAFVGFSY 487
QY 421 APPSEDLFL 429
Db 488 APPSEDLFL 496

RESULT 8
Q5ZJQ4_CHICK
ID Q5ZJQ4_CHICK PRELIMINARY; PRT; 490 AA.
AC Q5ZJQ4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.1698;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ702380; CAG32039.1; -; mRNA.
DR SMR; Q5ZJQ4; 4-119.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007422; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001683; PX.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00195; PX; 1.
KW Hypothetical protein.
SQ SEQUENCE 490 AA; 56260 MW; 756D6F95B3EB3F5 CRC64;

Query Match 94.3%; Score 2140; DB 2; Length 490;
Best Local Similarity 93.7%; Pred. No. 3e-131;
Matches 401; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALKIPAKRIFGNFDDFDFKQRRAGINEFIQNLVRYPELVNHPDVRFAFLQMDSPKHQSD 60
Db 62 MNLUKIPAKRIFGNFDDFDFKQRRAGINEFIQNLVRYPELVNHPDVRFAFLQMDSPKHQSD 121
QY 61 PSEDEDESSQKLHSTSQINLPGSNPHAKPTDFDFLVKVGSGFKVLLAKRKLKGK 120

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Db 122 PSEDEDESSQKLHSTSQINLPGSNPHAKPTDFDFLVKVGSGFKVLLAKRKLKGK 181
QY 121 YAKVLQKKLVLRKQKHIMAEARNVLLKNVHPFLVGLHYSQTTTEKLYFVLDPVNGGE 180
Db 182 YAKVLQKKLVLRKQKHIMAEARNVLLKNVHPFLVGLHYSQTTTEKLYFVLDPVNGGE 241
QY 181 LFFHLQERSFPEHRAFYAAEIASALGYLHLSIKIVYRDLKPNILDSVGHVVLTFDGL 240
Db 242 LFFHLQERSFPEHRAFYAAEIASALGYLHLSINIVYRDLKPNILDSVGHVVLTFDGL 301
QY 241 CKEGIASLDTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 300
Db 302 CKEGIASLDTTTCGTPPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPPYCRDVA 361
QY 301 EMDNIIHKPLSLRPGVSLTAWSTLELLEKDRNRLGAKEDFLEIQNHPPFESLSWADL 360
Db 362 EMDNIIHKPLSLRPGVSLTAWSTLELLEKDRNRLGAKEDFLEIQNHPPFESLSWADL 421
QY 361 VQKIPPPNPVAGPDIDRNFDTAFTEETVPYVSVSSDYIVNASVLEADDAFVGFSY 420
Db 422 LQKIPPPNPVAGPDIDRNFDTAFTEETVPYVSVSSDYIVNASVLEADDAFVGFSY 481
QY 421 APPSEDLFL 428
Db 482 APPSEDMF 489

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RESULT 9

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Q4SFC2_TETNG
ID Q4SFC2_TETNG PRELIMINARY; PRT; 518 AA.
AC Q4SFC2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 6 SCAF14605, whole genome shotgun sequence.
GN ORFNames=GSTENG00019161001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01014605; CAG00660.1; -; Genomic DNA.
SQ SEQUENCE 518 AA; 59656 MW; 4CF4E51FF8BA3E5 CRC64;

Query Match 78.6%; Score 1783; DB 2; Length 518;
Best Local Similarity 77.8%; Pred. No. 5.8e-108;
Matches 332; Conservative 45; Mismatches 46; Indels 4; Gaps 1;

```

QY 3 LKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQWDSFKHQSDPS 62
 Db LKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQWDSFKHQSDPS 155
 QY 63 EDEDERSSQKLHSTSONINLGPSPGNPHAKPTDFDLKVLGKSGFGKVLAKRLDKGFYA 122
 Db EDEDERSSQKLHSTSONINLGPSPGNPHAKPTDFDLKVLGKSGFGKVLAKRLDKGFYA 211
 QY 123 VYLQKQKIVLNKREKQKHMAERNVLLKNVHPFLVGLHYHSFQTEKLYFVLDFVNGGELF 182
 Db VYLQKQKIVLNKREKQKHMAERNVLLKNVHPFLVGLHYHSFQTEKLYFVLDFVNGGELF 271
 QY 183 FHLQERSFPEHRARFYAAIASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGLCK 242
 Db FHLQERSFPEHRARFYAAIASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGLCK 331
 QY 243 EGIAISDITTTFCGTPEYLAPEVRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEM 302
 Db EGIAISDITTTFCGTPEYLAPEVRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEM 391
 QY 303 YDNILHKPLSLRPGVSLTAWSIILELLEKDRQNLGAKEDFLBIONHPFFESLSWADLVQ 362
 Db YDNILHKPLSLRPGVSLTAWSIILELLEKDRQNLGAKEDFLBIONHPFFESLSWADLVQ 451
 QY 363 KKI1PPFPNPNVAGDDIRNFTDFTBETVPYSCVSDSYIVNASVLEADDAFVGFSYAP 422
 Db KKI1PPFPNPNVAGDDIRNFTDFTBETVPYSCVSDSYIVNASVLEADDAFVGFSYAP 511
 QY 423 PSEDLF 429
 Db PSEDLF 518

RESULT 10
 Q5YV65 HUMAN
 ID Q5YV65 HUMAN PRELIMINARY; PRT; 526 AA.
 AC Q5YV65;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE OTTHUMP0000017246
 GN Name=SGK; ORFNames=RP1-188K17.1-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall R.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Tracey A.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Milne S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AL355881; CA172579.1; -, Genomic DNA.
 DR ENBL; AL355839; CA119721.1; -, Genomic DNA.
 DR ENBL; Z84486; CA121678.1; -, Genomic DNA.
 DR ENBL; AL135839; CA172579.1; JOINED; Genomic DNA.
 DR ENBL; Z84486; CA172579.1; JOINED; Genomic DNA.
 DR ENBL; Z84486; CA119721.1; JOINED; Genomic DNA.
 DR ENBL; Z84486; CA119721.1; JOINED; Genomic DNA.
 DR ENBL; AL135839; CA121678.1; JOINED; Genomic DNA.
 DR ENBL; AL355881; CA121678.1; JOINED; Genomic DNA.
 DR Ensembl; ENSG00000118515; Homo sapiens.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase C; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Kinase.
 SQ SEQUENCE 526 AA; 59904 MW; 8CE1E9DFB949D5A5 CRC64;
 Query Match 66.2%; Score 1501; DB 2; Length 526;
 Best Local Similarity 66.8%; Pred. No. 1.4e-89;
 Matches 286; Conservative 52; Mismatches 76; Indels 14; Gaps 3;
 QY 6 PAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQWDSFKHQSDPS 61
 Db PAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQWDSFKHQSDPS 168
 QY 62 SEDEDERSSQKLHSTSONINLGPSPGNPHAKPTDFDLKVLGKSGFGKVLAKRLDKGFY 121
 Db SEDEDERSSQKLHSTSONINLGPSPGNPHAKPTDFDLKVLGKSGFGKVLAKRLDKGFY 219
 QY 122 AVKVLQKIVLNKREKQKHMAERNVLLKNVHPFLVGLHYHSFQTEKLYFVLDFVNGGEL 181
 Db AVKVLQKIVLNKREKQKHMAERNVLLKNVHPFLVGLHYHSFQTEKLYFVLDFVNGGEL 279
 QY 182 FHLQERSFPEHRARFYAAIASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGLC 241
 Db FHLQERSFPEHRARFYAAIASALGYLHSIKIVYRDLKPNILLDSVGHVLTDFGLC 339
 QY 242 KEGIAISDITTTFCGTPEYLAPEVRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAE 301
 Db KEGIAISDITTTFCGTPEYLAPEVRKOPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAE 399
 QY 302 MYDNILHKPLSLRPGVSLTAWSIILELLEKDRQNLGAKEDFLBIONHPFFESLSWADLV 361
 Db MYDNILHKPLSLRPGVSLTAWSIILELLEKDRQNLGAKEDFLBIONHPFFESLSWADLV 459
 QY 362 QKKIPFPNPNVAGDDIRNFTDFTBETVPYSCVSDSYIVNASVLEADDAFVGFSYA 421
 Db QKKIPFPNPNVAGDDIRNFTDFTBETVPYSCVSDSYIVNASVLEADDAFVGFSYA 519
 QY 422 PSEDLF 429
 Db PSEDLF 526
 RESULT 11
 Q5TCN4 HUMAN
 ID Q5TCN4 HUMAN PRELIMINARY; PRT; 421 AA.
 AC Q5TCN4;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE OTTHUMP0000017249
 GN Name=SGK; ORFNames=RP1-188K17.1-011;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tracey A.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

EMBL: AL135839; CA119718.1; -, Genomic_DNA.
GO: GO:0005524; F:ATP binding; IEA.
GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro: IPR000961; Pkinase_C.
InterPro: IPR000719; Prot_kinase.
InterPro: IPR008271; Ser_thr_pkin_AS.
InterPro: IPR002290; Ser_thr_pkinase.
InterPro: IPR001245; Tyr_pkinase.
Pfam: PF00069; Pkinase; 1.
Pfam: PF00433; Pkinase; 1.
ProDom: PD000001; Prot_kinase; 1.
SMART: SM00133; S_TK_X; 1.
SMART: SM00220; S_TKC; 1.
SMART: SM00219; TyrKc; 1.
PROSITE: PS00107; PROTEIN KINASE ATP; 1.
PROSITE: PS00111; PROTEIN KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN KINASE_ST; 1.
SEQUENCE 421 AA; 47910 MW; 6BDCD1FA7D9AFD0E CRC64;
Query Match 65.3%; Score 1482.5; DB 2; Length 421;
Best Local Similarity 66.0%; Pred. No. 1.8e-88;
Matches 285; Conservative 53; Mismatches 73; Indels 21; Gaps 5;
QY 6 PAKRIFGDNFDDP-----FIKORRAGLNEFIQNLVYPPELVNHPDVRAPFLQWDSPKH--- 57
DB 3 PSKRFF---ISPPSSTAFMKQRRMGLNDFIQKIANNVYACKHPVQSIKISQPEPELM 59
QY 58 QSDPSEDEDESSQKLHSTQNLGPGSNPHAKPTDFDLKVGKSGFKVLLAKRKL 117
DB 60 NAMPSPPP-----SPSQINLGPSSNPHAKPSDFHLKVGKSGFKVLLARHAE 110
QY 118 GKFAVAVKLOKIVLNRKEQKHIWAERNVLLKNVGHFLVGLHYSFOTTEKLYFVLDFVN 177
DB 111 EVFAVAVKLOKAILKKKEKHINSERNVLLKNVGHFLVGLHFSFOTADKLYFVLDFYN 170
QY 178 GGELFFHLQERSPEPRARFYAAEIASALGYLHSIKIVYRDLPENILDSVGHVVLTD 237
DB 171 GGELFYHLQERCFLEPRARFYAAEIASALGYLHSINIVYRDLPENILDSQGHVVLTD 230
QY 238 FGLCKEGIALSTTTTCGTPPEYLAPEVIRKQPDVNTVWCLGAVLYEMLYGLPPPYCR 297
DB 231 FGLCKENIEHSTSTFCGTPPEYLAPEVLRKQPDVNTVWCLGAVLYEMLYGLPPPYCR 290
QY 298 DVAEVYDNIHLKPLSLRPGVSLTAWSTLELLEKQDNRLGAKEDFLEIQNHPPFESLSW 357
DB 291 NTAEMYDNIHLKPLSLRPGVSLTAWSTLELLEKQDNRLGAKEDFLEIQNHPPFESLSW 350
QY 358 ADLVQKIPPPFPNPNVAGPDIDRFATFTETVPVSCVSSDYIVNASVLEADDAFVG 417
DB 351 DLLINKKITPPFPNPNVSGPDLRHFDPFTPEEPVPNSIGKSPDSVLVTASVKEAAEAFIG 410
QY 418 FSVAPSPEDLFL 429
DB 411 FSVAPPT-DSFL 421
RESULT 12
Q6NS85_MOUSE PRELIMINARY; PRT; 519 AA.
AC Q6NS85;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Sgk protein.
GN Sgk protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Phosphorylates a large number of substrates in the
cytoplasm and the nucleus (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and
monomeric catalytic subunit). Translocates into the nucleus
(monomeric catalytic subunit) (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL: BC070401; AAH70401.1; -, mRNA.
HSSP; P05132; 1ATP.
DR Ensembl; ENSMUSG00000019970; Mus musculus.
DR MGI; MGI:1340062; Sgk
GO: GO:0004672; P:protein kinase activity; IEA.
GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
GO: GO:0006974; P:response to DNA damage stimulus; IEA.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 519 AA; 58984 MW; BB79975BA911DEC3 CRC64;
Query Match 65.2%; Score 1480; DB 2; Length 519;
Best Local Similarity 66.6%; Pred. No. 3.3e-88;
Matches 285; Conservative 49; Mismatches 80; Indels 14; Gaps 3;
QY 6 PAKRIFGDNFDDPFIKORRAGLNEFIQNLVYPPELVNHPDVRAPFLQWDSPKH---QSDP 61
DB 102 PDPRTFTWTDAAAFMKQRRMGLNDFIQKIANNVYACKHAEVQSIKMSHPQPEPELMANP 161
QY 62 SEDEDESSQKLHSTQNLGPGSNPHAKPTDFDLKVGKSGFKVLLAKRKLCKFY 121
DB 162 SPPP-----SPSQINLGPSSNPHAKPSDFHLKVGKSGFKVLLARHAEVFF 212
QY 122 AVKVLQKIVLNRKEQKHIWAERNVLLKNVGHFLVGLHYSFOTTEKLYFVLDFVNGEL 181

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Db 213 AVKVLQKALKKKEKHGINSERNVLLKNVGHFLVGLHFSFQTADKLYFVLVDYINGGEL 272
Qy 182 FFHLQERSPEHRAFYAAEIASALGYLHSIKIVYRDLDKPENILLDSVGHVVLTDPLGLC 241
Db 273 FYHLQERCFLEPRARFYAAEIASALGYLHSINIVYRDLDKPENILLDSQGHIVLTDPLGLC 332
Qy 242 KEGIALSDTTTTCCGTPPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAE 301
Db 333 KENIEHNGTSTTCGTPPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAE 392
Qy 302 MYDNLHKPLSLRPGVSLTAWSLTELELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLV 361
Db 393 MYDNLKPLQLKPNITNSARHLLGGLLKQDKTRKLGAKDDFNEIKSHIFFSLLINWDDLI 452
Qy 362 QKKIPFPNPNVAGPDIDRNFDTAFTTEVPYSCVSSDYSIVNASVLEADDAFVGFSYA 421
Db 453 NKKITPPFNPNVSGPSDLRHFDPFTEEPVPSIGRSPDSILVTASVKEAAEAFLGFSYA 512
Qy 422 PPSDELFL 429
Db 513 PP-VDSFL 519
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RESULT 13

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Q5TCN3_HUMAN
ID Q5TCN3_HUMAN PRELIMINARY; PRT; 431 AA.
AC Q5TCN3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE OTTHUMP00000017247.
GN Name=SGK; ORFNames=RP1-188K17.1-009;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tracay A.;
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL135839; CAT19719.1; -; Genomic_DNA.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase C.1.
DR Pfam; PF00433; Pkinase C.1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 431 AA; 48942 MW; F3697C63AB1F499D CRC64;
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Query Match 65.1%; Score 1476; DB 2; Length 431;
Best Local Similarity 67.5%; Pred. No. 4.8e-88;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
Qy 19 FIKQRAGLNEFTQNLVRYPELVNHPDVRAFLQWDSPKH----QSDPSDEDSRSQKLH 74
Db 27 FMKQRRLGNLDFIQKIANNSSYACKHPEVOSILKISQFPELMNANPSPPP----- 77
Qy 75 STSQINILGSGNPHAKPTDFDLKVIKGSGFGKVLAKRKLKDKFYAVKVLQKKTIVLNR 134
Db 78 SPSSQINLGSSNPHAKPSDFHLKVIKGSGFGKVLARHKAEEVYAVKVLQKALKKK 137
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Qy 135 KEQKIMABRNVLKNVGHFPLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQERSFPPEH 194
Db 138 KEEKHIMSRNVLKNVGHFPLVGLHFSFQTADKLYFVLVDYINGGELFFHLQERCFLEP 197
Qy 195 RARFYAAEIASALGYLHSIKIVYRDLDKPENILLDSVGHVVLTDPLGLCKEGIAISDTTTF 254
Db 198 RARFYAAEIASALGYLHSINIVYRDLDKPENILLDSQGHIVLTDPLGLCKENIEHSTSTTF 257
Qy 255 CQTPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNLHKPLSLR 314
Db 258 CQTPEYLAPVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNLHKPLQLK 317
Qy 315 PGVSLTAWSLTELELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKKIPFPNPNVA 374
Db 318 PNITNSARHLLGGLLKQDKTRKLGAKDDFNEIKSHIFFSLLINWDDLIINKKITPPFPNVS 377
Qy 375 GPDDIRNFDTAFTTEVPYSCVSSDYSIVNASVLEADDAFVGFSYAPPSDELFL 429
Db 378 GPNDLRHFDPEFTEEPVPSIGRSPDSVLTASVKEAAEAFLGFSYAPPT-DSFL 431

RESULT 14
Q68G05_RAT
ID Q68G05_RAT PRELIMINARY; PRT; 431 AA.
AC Q68G05;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Serum/glucocorticoid regulated kinase.
GN Name=SGK;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078843; AAH78843.1; -; mRNA.
DR Ensembl; ENSRNOG00000011815; Rattus norvegicus.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
```

DR InterPro; IPR008271; Ser_thr_pkin AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; Ty_KC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 431 AA; 49024 MW; 35261E7AC839CB3P CRC64;

Query Match 65.1%; Score 1476; DB 2; Length 431;
Best Local Similarity 67.7%; Pred. No. 4.8e-88;
Matches 28; Conservative 50; Mismatches 70; Indels 14; Gaps 3;

QY 19 FIKRRAGLNEFIQNLVRYPELVNHPDVRAPFLQWDSPKH---QSDPSEDEDERSSQKLH 74
DB 27 FMKQRRMGLNDFIQKLANNSVACKHPEVQSYLKISQPEPELMNANSPPP----- 77

QY 75 STSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFYAVKVLQKKIVLNR 134
DB 78 SPSQOINLGPSSNPHAKPSDFHFLKVIKGSFGKVLARHAKAEAFYAVKVLQKKAILKK 137

QY 135 KEQKHMAERNVLLKNVGHPLVGLHYSFQTTTEKLYFVDFVNGGELFFHLQERSPEH 194
DB 138 KEKHIMSERNVLLKNVGHPLVGLHFSFQTADKLYFVLDYINGGELFYHLQERCFLP 197

QY 195 RARFYAAEIASALGYLHSIKIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254
DB 198 RARFYAAEIASALGYLHSINIVYRDLPENILDSQGHIVLTDFGLCKENIEHNTSTF 257

QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNILHKPLSLR 314
DB 258 CGTPEYLAPEVIRKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYDNILKPLQLK 317

QY 315 PGVSLTAWSLTEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374
DB 318 PNITNSARHLLEGLLQKORTKRLGAKDDFMEIKSHIFFSLINWDDLLINKKITPPFPNVS 377

QY 375 GPDDIRNFDFTAFTEETVPYSCVSSDYISVNASVLEADDADFVGSFVAPPSEDLFL 429
DB 378 GPSDLRHFDEFTPEEPVPSSIGRSPDSILVTASVKEAAEAFVGSFVAPPDM-DSFL 431

RESULT 15
Q5TCN2 HUMAN
ID Q5TCN2 HUMAN PRELIMINARY; PRT; 445 AA.
AC Q5TCN2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE OTTHUMP0000017248.
GN Name=SGK; ORFNames=RP1-188K17.1-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted
DR EMBL; ALI35839; CAI19720.1; -; Genomic DNA.
DR Ensembl; ENSG00000118515; Homo sapiens.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.

DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; Ty_KC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
SQ SEQUENCE 445 AA; 50623 MW; DC7076E1F43BCBAB CRC64;

Query Match 65.1%; Score 1476; DB 2; Length 445;
Best Local Similarity 67.5%; Pred. No. 5e-88;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

QY 19 FIKRRAGLNEFIQNLVRYPELVNHPDVRAPFLQWDSPKH---QSDPSEDEDERSSQKLH 74
DB 41 FMKQRRMGLNDFIQKLANNSVACKHPEVQSYLKISQPEPELMNANSPPP----- 91

QY 75 STSQINILGPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKFYAVKVLQKKIVLNR 134
DB 92 SPSQOINLGPSSNPHAKPSDFHFLKVIKGSFGKVLARHAKAEAFYAVKVLQKKAILKK 151

QY 135 KEQKHMAERNVLLKNVGHPLVGLHYSFQTTTEKLYFVDFVNGGELFFHLQERSPEH 194
DB 152 KEKHIMSERNVLLKNVGHPLVGLHFSFQTADKLYFVLDYINGGELFYHLQERCFLP 211

QY 195 RARFYAAEIASALGYLHSIKIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 254
DB 212 RARFYAAEIASALGYLHSINIVYRDLPENILDSQGHIVLTDFGLCKENIEHNTSTF 271

QY 255 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNILHKPLSLR 314
DB 272 CGTPEYLAPEVIRKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYDNILKPLQLK 331

QY 315 PGVSLTAWSLTEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 374
DB 332 PNITNSARHLLEGLLQKORTKRLGAKDDFMEIKSHIFFSLINWDDLLINKKITPPFPNVS 391

QY 375 GPDDIRNFDFTAFTEETVPYSCVSSDYISVNASVLEADDADFVGSFVAPPSEDLFL 429
DB 392 GPSDLRHFDEFTPEEPVPSSIGRSPDSILVTASVKEAAEAFVGSFVAPPDM-DSFL 445

Search completed: January 27, 2006, 23:31:07
Job time : 70.8811 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:06:05 ; Search time 76.0006 Seconds
(without alignments)
2468.595 Million cell updates/sec

Title: US-09-868-131A-8

Perfect score: 2311

Sequence: 1 MQGLLTSGRRKPSGGRCRGR.....ASSAFLGFSYAPDDDDILDC 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	100.0	427	3	AAY95276 Human ser
2	2311	100.0	427	8	ADQ88284 Human 549
3	2124.5	91.9	398	6	ADA05780 Human NOV
4	2094.5	90.6	398	8	ADN62944 Human NOV
5	2005	86.8	382	4	AAM25594 Human pro
6	2005	86.8	396	9	ADY37607 Lung canc
7	1954	84.6	367	3	AAY95275 Human ser
8	1954	84.6	367	4	AAU28087 Novel hum
9	1954	84.6	367	5	AAE22765 Human ser
10	1954	84.6	367	7	ADD45799 Human Pro
11	1954	84.6	367	8	ADI29317 Human MAR
12	1954	84.6	367	8	ADJ45521 LXR-ligan
13	1952	84.5	367	4	AAB65708 Novel pro
14	1848	80.0	367	3	AAY95277 Mouse ser
15	1848	80.0	367	7	ADD45797 Rat Prote
16	1691	73.2	319	4	AAB99838 AGC prote
17	1691	73.2	319	8	ADJ38886 SGK2 amin
18	1677	72.6	335	8	ADP29822 Human sec
19	1665	72.0	330	8	ADN61463 Human Kpp
20	1435.5	62.1	788	7	ADD93289 p53-SGK(6
21	1420	61.4	431	3	AAB24116 Rat serum
22	1420	61.4	431	3	AAY93530 A rat ser
23	1419	61.4	407	7	ADC69794 Human ser
24	1419	61.4	431	2	AAW90139 Human sgk

25	1419	61.4	431	6	ADA10889	Ada10889 Human cdn
26	1419	61.4	431	7	ADG31708	Adg31708 Human pro
27	1419	61.4	431	7	ADK50982	Adk50982 Human NOV
28	1419	61.4	431	7	ADK50984	Adk50984 Human NOV
29	1419	61.4	431	8	ADO55118	Ado55118 Protein #
30	1419	61.4	431	9	ADY14632	Ady14632 PRO polyp
31	1419	61.4	431	9	ADY19878	Ady19878 PRO polyp
32	1419	61.4	431	9	AEA04529	Aea04529 Human pro
33	1419	61.4	442	7	ADG31706	Adg31706 Human pro
34	1419	61.4	445	7	ADC69792	Adc69792 Human pro
35	1419	61.4	526	6	ADA54293	Ada54293 Human pro
36	1419	61.4	526	7	ADG31710	Adg31710 Human pro
37	1416	61.3	431	8	ADO60030	Ado60030 CRH signa
38	1416	61.3	431	8	ADO44573	Ado44573 Serum/glu
39	1415	61.2	430	2	ADN95921	Adn95921 Human BEC
40	1415	61.2	431	2	AAW77217	Aaw77217 Human cel
41	1415	61.2	431	3	AAY95279	Aay95279 Human ser
42	1415	61.2	431	3	AAB24115	Aab24115 Human ser
43	1415	61.2	431	4	AAB65613	Aab65613 Novel pro
44	1415	61.2	431	7	ADD14174	Add14174 Human src
45	1415	61.2	431	7	ADE31655	Ade31655 Human 290

ALIGNMENTS

RESULT 1
AAY95276
ID AAY95276 standard; protein; 427 AA.
AC AAY95276;
XX
DT 12-SEP-2000 (first entry)
XX
DE Human serum and glucocorticoid-induced protein kinase 2-beta.
XX
KW Serum and glucocorticoid-induced protein kinase 2; SGK2-beta; human;
KW phosphorylation; cancer; diabetes; ischaemia; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 339
FT /note= "O-phosphorylated"
FT Modified-site 394
FT /note= "O-phosphorylated"
XX
PN WO200035946-A1.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-GB004232.
XX
PR 14-DEC-1998; 98US-0112217P.
PR 19-AUG-1999; 99GB-00019676.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Cohen P, Kobayashi T, Deak M;
XX
DR WPI; 2000-442364/38.
XX
DR N-PSDB; AAA27857.
XX
PT Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)
PT or dephosphorylation, useful for treatment of cancer, diabetes and
XX ischemic diseases.
XX
PS Disclosure; Page 6-7; 127pp; English.
XX
CC The present sequence is that of human serum and glucocorticoid-induced
CC protein kinase (SGK) isoform 2-beta. SGK (see AAY95279) was initially
CC identified as a glucocorticoid and osmotic stress-responsive gene. Novel

CC isoforms, SGK2 and SGK3, were isolated from EST database searches, and 2
CC splice variants of SGK2, i.e. SGK2-beta and -alpha (see AY95275), which
CC contains 60 fewer N-terminal residues, were identified. SGK2-beta is
CC expressed in liver and kidney. It is activated by phosphorylation in a
CC similar manner to SGK. The invention provides methods of activating SGK
CC activity by phosphorylation using 3-phosphoinositide-dependent protein
CC kinase-1 (PDK1), and of reducing the activity of SGK by
CC dephosphorylation. The invention also provides a method of identifying a
CC compound that modulates the activity of SGK. Such compounds are useful
CC for treating patients requiring modulation of SGK, such as patients with
CC cancer, diabetes or ischaemic disease
XX
SQ Sequence 427 AA;

Query Match 100.0%; Score 2311; DB 3; Length 427;
Best Local Similarity 100.0%; Pred. NO. 1.6e-202;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQGLLTSGRKPSGGGRCCTGRGGWRCQCLKPMWGGADPPTTSLCLLPVPPPLPDHCYR 60
Db 1 MQGLLTSGRKPSGGGRCCTGRGGWRCQCLKPMWGGADPPTTSLCLLPVPPPLPDHCYR 60
Qy 61 MNSSPAGTSPQPSRANGINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDFGAF 120
Db 61 MNSSPAGTSPQPSRANGINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDFGAF 120
Qy 121 YAVKVLQKSIKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 180
Db 121 YAVKVLQKSIKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 180
Qy 181 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240
Db 181 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240

Qy 241 CKEGVEPEDTSTFCGTPEYLAPEVLKKEPYDRAVDWMCILGAVLYEMLHGLPFPYSDVS 300
Db 241 CKEGVEPEDTSTFCGTPEYLAPEVLKKEPYDRAVDWMCILGAVLYEMLHGLPFPYSDVS 300
Qy 301 QMYENILHQPQIPGGRTVAACDLQLLHKDQRLGSKADFLKINHVFFSPINWDDL 360
Db 301 QMYENILHQPQIPGGRTVAACDLQLLHKDQRLGSKADFLKINHVFFSPINWDDL 360
Qy 361 YHKLRLTPPNPNVTGPADLKHDFPEFTQEAUSKISGCTPDTVASSGASSAFILGFSVAPE 420
Db 361 YHKLRLTPPNPNVTGPADLKHDFPEFTQEAUSKISGCTPDTVASSGASSAFILGFSVAPE 420
Qy 421 DDDILDC 427
Db 421 DDDILDC 427

RESULT 2
ADQ88284
ID ADQ88284 standard; protein; 427 AA.

XX ADQ88284;
AC ADQ88284;
XX 21-OCT-2004 (first entry)

XX Human 54946 protein, a Ser/Thr protein kinase SGK2.
DE human; cardiovascular disorder; thrombotic disorder;
KW differential expression; gene therapy; aberrant vascularisation;
KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;
KW dyslipidaemia; high blood pressure; heart failure; cardiac;
KW thrombolytic; anticoagulant; antilipaeamic; hypotensive; cardiac;
KW Ser/Thr protein kinase; SGK2; EC 2.7.1.37; enzyme.

XX Homo sapiens.
XX WO2004063340-A2.
XX 29-JUL-2004.
PD

XX 13-JAN-2004; 2004WO-US000393.
PF
XX 13-JAN-2003; 2003US-0439683P.
PR 05-FEB-2003; 2003US-0445216P.
PR 18-FEB-2003; 2003US-0448036P.
PR 12-MAR-2003; 2003US-0454189P.
PR 25-MAR-2003; 2003US-0457541P.
PR 29-APR-2003; 2003US-0466411P.
PR 08-MAY-2003; 2003US-0469041P.
PR 10-JUN-2003; 2003US-0477414P.
PR 24-JUL-2003; 2003US-0478560P.
PR 13-AUG-2003; 2003US-0489772P.
PR 28-JUL-2003; 2003US-0490660P.
PR 03-SEP-2003; 2003US-0499838P.
PR 22-SEP-2003; 2003US-0504786P.
PR 24-SEP-2003; 2003US-0505570P.
PR 17-OCT-2003; 2003US-0512418P.
PR 27-OCT-2003; 2003US-0514660P.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;
PI Rogrigue-Way A, Tomlinson JE;
PI WPI; 2004-553729/53.
DR N-PSDB; ADQ88283.

PT Identifying a compound for treating a cardiovascular or thrombotic
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
PT and detecting the binding.
XX

PS Claim 1; SEQ ID NO 126; 512pp; English.

XX This invention relates to a novel compound that is capable of treating a
CC cardiovascular or thrombotic disorder. Specifically, it refers to the
CC identification of nucleic acid molecules, and the encoded proteins
CC thereof, which are differentially expressed in cardiovascular disease
CC states relative to their normal expression in non-diseased tissue. The
CC present invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of
CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation,
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,
CC dyslipidaemia, high blood pressure or heart failure. As such, they
CC exhibit cardiac, thrombolytic, anticoagulant, antilipaeamic, hypotensive
CC and cardiac activities. This polypeptide sequence is a human protein
CC that is differentially expressed in a patient with a cardiovascular
CC disorder, given in an exemplification of the invention.

XX SQ Sequence 427 AA;

Query Match 100.0%; Score 2311; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. NO. 1.6e-202;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQGLLTSGRKPSGGGRCCTGRGGWRCQCLKPMWGGADPPTTSLCLLPVPPPLPDHCYR 60
Db 1 MQGLLTSGRKPSGGGRCCTGRGGWRCQCLKPMWGGADPPTTSLCLLPVPPPLPDHCYR 60
Qy 61 MNSSPAGTSPQPSRANGINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDFGAF 120
Db 61 MNSSPAGTSPQPSRANGINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRKSDFGAF 120
Qy 121 YAVKVLQKSIKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 180
Db 121 YAVKVLQKSIKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYNGGE 180
Qy 181 LFFHLQRRERFLEPRARFYAAEVAASIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240

Db 181 LFFHLQRRERFLEPRAFYAASVATGYLHSLNIIYRDLKPEINILDCQGHVVLTDFGL 240
Qy 241 CKGEVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFYSDVS 300
Db 241 CKGEVEPEDTTSTFCGTPPEYLAPEVLKPEYDRAVDWVCLGAVLYEMLHGLPPFYSDVS 300
Qy 301 QMYENILHQLIPIGGRVTAACDLQLSLHKKQORLGSKADFLFIKNHVFVFFSPINWDDL 360
Db 301 QMYENILHQLIPIGGRVTAACDLQLSLHKKQORLGSKADFLFIKNHVFVFFSPINWDDL 360
Qy 361 YHKELTPPENVTGPADLKHFDPEFTQEAIVSKIGCTPTDVASSGASSAFLGFSVAPE 420
Db 361 YHKELTPPENVTGPADLKHFDPEFTQEAIVSKIGCTPTDVASSGASSAFLGFSVAPE 420
Qy 421 DDDILDC 427
Db 421 DDDILDC 427

RESULT 3

ADA05780
ID ADA05780 standard; protein; 398 AA.

AC ADA05780;

DT 06-NOV-2003 (first entry)

XX Human NOV33a protein SEQ ID NO:140.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX Homo sapiens.

XX WO2003029424-A2.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327435P.

XX 09-OCT-2001; 2001US-0327917P.

XX 09-OCT-2001; 2001US-0328029P.

XX 09-OCT-2001; 2001US-0328044P.

XX 12-OCT-2001; 2001US-0328849P.

XX 15-OCT-2001; 2001US-0329414P.

XX 17-OCT-2001; 2001US-0330142P.

XX 18-OCT-2001; 2001US-0330309P.

XX 24-OCT-2001; 2001US-0339266P.

XX 29-OCT-2001; 2001US-0343629P.

XX 01-NOV-2001; 2001US-0349575P.

XX 17-APR-2002; 2002US-0346357P.

XX 19-APR-2002; 2002US-0373815P.

XX 19-APR-2002; 2002US-0373817P.

XX 19-APR-2002; 2002US-0373826P.

XX 19-APR-2002; 2002US-0373884P.

XX 16-MAY-2002; 2002US-0374977P.

XX 16-MAY-2002; 2002US-0381037P.

XX 16-MAY-2002; 2002US-0381038P.

XX 16-MAY-2002; 2002US-0381042P.

XX 17-MAY-2002; 2002US-0381642P.

XX 28-MAY-2002; 2002US-0383656P.

XX 29-MAY-2002; 2002US-0383831P.

XX 25-JUN-2002; 2002US-0391335P.

PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;

PI Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CB, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;

PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

DR N-PSDB; ADA05779.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing,

PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,

PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or

XX pharmacogenomics.

XX Claim 1; Page 219; 586pp; English.

XX The present invention describes NOVX proteins, where X can be 1 to 55

CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

CC described above and a carrier; (2) a kit comprising, in one or more

CC containers, the composition described above; (3) an isolated nucleic acid

CC molecule which encodes a NOVX protein of the invention; (4) a vector

CC comprising the nucleic acid molecule described above; (5) a cell

CC comprising the above vector; (6) an antibody that immunospecifically

CC binds to the polypeptide described above; (7) methods for determining the

CC presence or amount of the above polypeptide or nucleic acid molecule in a

CC sample; (8) methods for determining the presence of or predisposition to

CC a disease associated with altered levels of expression of the above

CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a

CC method of identifying an agent that binds to the polypeptide described

CC above; (10) a method for identifying a potential therapeutic agent for

CC use in treating a pathology that is related to an aberrant expression or

CC aberrant physiological interactions of the polypeptide; (11) a method of

CC screening for a modulator of activity or of latency or predisposition to

CC a pathology associated with the polypeptide; (12) a method for modulating

CC or preventing a pathology associated with the above polypeptide in a

CC mammal; and (14) a method for producing the above polypeptide. NOVX

CC sequences have antidiabetic, anorectic, antibacterial, virucide,

CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian

CC and antilipemic activities, and can be used in gene therapy. The

CC polypeptide is useful in manufacturing a medicament for treating a

CC syndrome associated with a human disease. The polypeptide or the nucleic

CC acid molecule may be used to diagnose, treat or prevent metabolic

CC disorders such as diabetes or obesity, infections, cachexia, cancer,

CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various

CC dyslipidaemias. The nucleic acids can also be used as hybridisation

CC probes, in chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. The present sequence represents a human NOVX from the

XX present invention.

SQ Sequence 398 AA;

Query Match 91.9%; Score 2124.5; DB 6; Length 398;
Best Local Similarity 93.2%; Pred. No. 1.8e-185;
Matches 398; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MQGLLTSGRKPSGGGRCGTGGRGWGQWCLKPNWGGADPPTTLLPPELPDHCYR 60
Db 1 MQGLLTSGRKPSGGGRCGTGGRGWGQWCLKPNWGGADPPTTLLPPELPDHCYR 60
QY 61 MNSSPAGTSPQPSRANGINILGFSANPNAQPTDFDLKVIKGNKGKVLAKRKSDGAF 120
Db 61 MNSSPAGTSPQPSRANGINILGFSANPNAQPTDFDLKVIKGNKGKVLAKRKSDGAF 120
QY 121 YAVKVLQKKSILKKKESQSHIMAERSVLLKNVRHFFVLGLRYSFQTPEKLYFVLDYNGGE 180
Db 121 YAVKVLQKKSILKKKESQSHIMAERSVLLKNVRHFFVLGLRYSFQTPEKLYFVLDYNGGE 180

QY 181 LFFHLQRRERFLEPRARFYAAEVAASAIGYLHLSNIIYRDLKPNILLDCQHVVLTFDGL 240
DB 181 LFFHLQRRERFLEPRARFYAAEVAASAIGYLHLSNIIYRDLKPNILLDCQ----- 230
QY 241 CKEGVEPEDTTSTFCGTPEYLAPEVLKPEPYDRAVDWVCIGAVLYEMLHGLPPFYSQDVS 300
DB 231 -----YLAPEVLKPEPYDRAVDWVCIGAVLYEMLHGLPPFYSQDVS 271
QY 301 QMYENILHOPLOIPGGRVAAACDLQSLHLKQORGLGSKADPLEIKNVHFFSPINWDDL 360
DB 272 QMYENILHOPLOIPGGRVAAACDLQSLHLKQORGLGSKADPLEIKNVHFFSPINWDDL 331
QY 361 YHKRLTPPNPNVTGADLKHDFPEFTQEAHSVKSIGCTPDTVASSGASSAFIGFSYAPE 420
DB 332 YHKRLTPPNPNVTGADLKHDFPEFTQEAHSVKSIGCTPDTVASSGASSAFIGFSYAPE 391
QY 421 DDDILDC 427
DB 392 DDDILDC 398
RESULT 4
ADN62944
ID ADN62944 standard; protein; 398 AA.
XX ADN62944;
AC
XX
DT 01-JUL-2004 (first entry)
XX Human NOV33a.
DE
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.

PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATI/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (ROTH/) ROTHENBERG R A.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62943.
DR
XX
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
PT
XX
PS Claim 1; SEQ ID NO 140; 395pp; English.
PS
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,

CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, immunodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 398 AA;

Query Match 90.6%; Score 2094.5; DB 8; Length 398;
Best Local Similarity 92.3%; Pred. No. 9.8e-183;
Matches 394; Conservative 1; Mismatches 3; Indels 29; Gaps 1;

QY 1 MOGLTSGRPSGGRCCTGRGWRGQCLKPMWGDADPTTSLCLLPVPPPELDHCYR 60
DB 1 MOGLTSGRPSGGRCCTGRGWRGQCLKPMWGDADPTTSLCLLPVPPPELDHCYR 60
QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAPQPTDFDLKVLGKNGYGVLLAKKSDGAF 120
DB 61 MNSSPAGTSPQPSRANGNINLGPSANPNAPQPTDFDLKVLGKNGYGVLLAKKSDGAF 120
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLDYVNGE 180
DB 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFOTPEKLYFVLDYVNGE 180
QY 181 LFPHLOERFLEPRAPFYAAEVAASATGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240
DB 181 LFPHLOERFLEPRAPFYAAEVAASATGYLHSLNIIYRDLKPNILLDCQ----- 230
QY 241 CKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPVDRADVWCLGAVLYEMLHGLPPFYSQDV 300
DB 231 -----YLAPEVLRKEFVDRADVWCLGAVLYEMLHGLPPFYSQDV 271
QY 301 QMVENILHQLPIPGGRTVAACDLQLSLHKKQRLGSKADFLKIKNVHFFSPINWDDL 360
DB 272 QMVENILHQLPIPGGRTVAACDLQLSLHKKQRLGSKADFLKIKNVHFFSPINWDDL 331
QY 361 YHKLTPPPNPNTGPADLKHDFEFTQEAUVSKSIGCTPTDVASSGSAFGLGFSYAPE 420
DB 332 YHKLTPPPNPNTGPADLKHDFEFTQEAUVSKSIGCTPTDVASSGSAFGLGFSYAPE 391
QY 421 DDILDC 427
DB 392 DDILDC 398

RESULT 5

AAM25594

ID AAM25594 standard; protein; 382 AA.

XX AC AAM25594;

XX 16-OCT-2001 (first entry)

DT Human protein sequence SEQ ID NO:1109.

DE

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

KW anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;

KW antibacterial; endocrine; cardiac; central nervous system; virucide;

KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;

KW dermatological; antiallergic; antiaethmatic; antidiabetic; cystostatic;

KW neuroprotective; antidepressant; antitropic; antiparkinsonian; infection;

KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;

KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

KW genetic disease; haematopoietic disorder; platelet disorder; asthma;

KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

KW allergic rhinitis; diabetes; multiple sclerosis; depression;

KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;

KW neurodegenerative disorder.

XX

OS Homo sapiens.

XX WO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000MO-US035017.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457603/49.

XX N-PSDB; AAH99535.

XX Isolated human polynucleotides encoding polypeptides, useful for the

XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX Claim 20; Page 227; 1217pp; English.

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to

XX AAM25963. The proteins can have activities based on the tissues and cells

XX they are expressed in, such as: antiinflammatory; antirheumatic;

XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;

XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;

XX cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;

XX antiulcer; osteopathic; dermatological; antiallergic; antiaethmatic;

XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;

XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides

XX encoding them can be used in gene therapy, antisense therapy and vaccine

XX production. The proteins and polynucleotides are useful for screening for

XX agonists or antagonists of a protein and for the treatment and diagnosis

XX of disorders associated with the activity of a protein e.g. inflammation,

XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,

XX neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal

XX infections, autoimmunity, genetic diseases, haematopoietic disorders,

XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,

XX osteoporosis, severe combined immunodeficiency, eczema, allergic

XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,

XX Alzheimer's disease, Parkinson's disease, neurodegenerative and

XX neurological disorders

XX SQ Sequence 382 AA;

Query Match 86.8%; Score 2005; DB 4; Length 382;

Best Local Similarity 100.0%; Pred. No. 1.5e-174;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 ELPDHCYRMNSPAGTSPQPSRANGNINLGPSANPNAPQPTDFDLKVLGKNGYGVLLA 112

DB 8 ELPDHCYRMNSPAGTSPQPSRANGNINLGPSANPNAPQPTDFDLKVLGKNGYGVLLA 67

QY 113 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFOTPEKLYFV 172

DB 68 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFOTPEKLYFV 127

QY 173 LDVYNGGELFPHLOERRRFLPRAPFYAAEVAASATGYLHSLNIIYRDLKPNILLDCQGH 232

DB 128 LDVYNGGELFPHLOERRRFLPRAPFYAAEVAASATGYLHSLNIIYRDLKPNILLDCQGH 187

QY 233 VVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPVDRADVWCLGAVLYEMLHGLP 292

DB 188 VVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPEVLRKEPVDRADVWCLGAVLYEMLHGLP 247

QY 293 PFYSQDVSMYENILHQLPIPGGRTVAACDLQLSLHKKQRLGSKADFLKIKNVHFF 352

DB 248 PFYSQDVSMYENILHQLPIPGGRTVAACDLQLSLHKKQRLGSKADFLKIKNVHFF 307

```
QY 353 SPINWDDLYHKRLTTPPNPNVTGPADLKHDFDPFTQEAHSVKSIGCTPDTTVASSSGASSAF 412
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 308 SPINWDDLYHKRLTTPPNPNVTGPADLKHDFDPFTQEAHSVKSIGCTPDTTVASSSGASSAF 367
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 413 LGFSYAPEDDDDDILDC 427
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
368 LGFSYAPEDDDDDILDC 382

RESULT 6
ADY37607
ID ADY37607 standard; protein; 396 AA.
XX
AC ADY37607;
XX
DT 19-MAY-2005 (first entry)
DE Lung cancer related protein, SEQ ID 83.
XX
KW Cytostatic; lung tumor.
XX
OS Homo sapiens.
XX
PN US2005048589-A1.
XX
PD 03-MAR-2005.
XX
PF 25-AUG-2004; 2004US-00926543.
XX
PR 25-AUG-2003; 2003US-0497790P.
XX
PA (JEND/) JENDOUBI M.
XX
PI Jendoubi M;
XX
DR WPI; 2005-221517/23.
DR N-PSDB; ADY37561.
XX
FT New antibody specific for an antigen differentially expressed between
FT lung cancer tissue and normal tissue, useful for diagnosing, treating or
FT preventing lung cancer.
XX
PS Disclosure; SEQ ID NO 83; 171pp; English.
XX
CC The present invention relates to an antibody (I) that binds to an antigen
CC that is differentially expressed between lung cancer tissue and normal
CC tissue, where the antigen is encoded by ADY37525. Also disclosed are
CC polypeptides (ADY37573-ADY37618) encoded by lung cancer related genes
CC (ADY37525-ADY37572), their fragments, analogs or derivatives; producing
CC lung cancer related polypeptides; and a diagnostic kit for detection and
CC disease management of lung cancer. (I) is useful for characterizing and
CC analyzing biological activity and function of the lung cancer-specific
CC gene products in relation to cellular pathways and networks in normal and
CC disease states, purifying the cancer specific gene products, and
CC detecting lung cancer-specific gene products and their expression levels
CC in animal models of cancer. (I) is also useful for diagnosing, treating
CC or preventing lung cancer, and also disorders related to abnormal
CC cellular differentiation, proliferation or degeneration.
XX
SQ Sequence 396 AA;

Query Match 86.8%; Score 2005; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.5e-174;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 ELPDHCYRMNNSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVLIA 112
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
22 ELPDHCYRMNNSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVLIA 81

QY 113 KRKSDGAFYAVKVLQKKSLKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPEKLYFV 172
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
82 KRKSDGAFYAVKVLQKKSLKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPEKLYFV 141
```

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QY 173 LDYVNGGELFFHLQRRERLEPRARYAAEVAISAICYLHSLNIIVRDLKPENILLDCQGH 232
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
142 LDYVNGGELFFHLQRRERLEPRARYAAEVAISAICYLHSLNIIVRDLKPENILLDCQGH 201
QY 233 VVLTDGFLCKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLP 292
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
202 VVLTDGFLCKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLP 261
QY 293 PFYSQDVSMYENILHQPLQIPGGRTVAACDQLLSLLHKDQORQLGSKADFLFIKNHVPF 352
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
262 PFYSQDVSMYENILHQPLQIPGGRTVAACDQLLSLLHKDQORQLGSKADFLFIKNHVPF 321
QY 353 SPINWDDLYHKRLTTPPNPNVTGPADLKHDFDPFTQEAHSVKSIGCTPDTTVASSSGASSAF 412
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
322 SPINWDDLYHKRLTTPPNPNVTGPADLKHDFDPFTQEAHSVKSIGCTPDTTVASSSGASSAF 381
QY 413 LGFSYAPEDDDDDILDC 427
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
382 LGFSYAPEDDDDDILDC 396

RESULT 7
AA95275
ID AA95275 standard; protein; 367 AA.
XX
AC AA95275;
XX
DT 12-SEP-2000 (first entry)
DE Human serum and glucocorticoid-induced protein kinase 2-alpha.
XX
KW Serum and glucocorticoid-induced protein kinase 2; SGK2-alpha; human;
KW phosphorylation; cancer; diabetes; ischaemia; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 279
FT Modified-site /note= "O-phosphorylated"
FT Modified-site 334
FT Modified-site /note= "O-phosphorylated"
XX
PN WO200035946-A1.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-GB004232.
XX
PR 14-DEC-1998; 98US-0112217P.
PR 19-AUG-1999; 99GB-00019676.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Cohen P, Kobayashi T, Deak M;
XX
XX WPI; 2000-442364/38.
DR N-PSDB; AAA27856.
XX
PT Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)
PT or dephosphorylation, useful for treatment of cancer, diabetes and
PT ischemic diseases.
XX
PS Disclosure; Page 6; 127pp; English.
XX
CC The present sequence is that of human serum and glucocorticoid-induced
CC protein kinase (SGK) isoform 2-alpha. SGK (see AA95279) was initially
CC identified as a glucocorticoid and osmotic stress-responsive gene. Novel
CC isoforms, SGK2 and SGK3, were isolated from EST database searches, and 2
CC splice variants of SGK2, i.e. SGK2-alpha and -beta (see AA95276), which
CC contains an extra 60 N-terminal residues, were identified. SGK2-alpha is
CC expressed in liver, kidney, pancreas and brain. It is activated by
CC phosphorylation in a similar manner to SGK. The invention provides
```

CC methods of activating SGK activity by phosphorylation using 3-phosphoinositide-dependent protein kinase-1 (PDK1), and of reducing the activity of SGK by dephosphorylation. The invention also provides a method of identifying a compound that modulates the activity of SGK. Such compounds are useful for treating patients requiring modulation of SGK, such as patients with cancer, diabetes or ischaemic disease

XX Sequence 367, AA;

Query Match 84.6%; Score 1954; DB 3; Length 367;
Best Local Similarity 100.0%; Pred. No. 6.5e-170;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 MNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVGKNGYKVLAKRKSQDGF 120
Db 1 MNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVGKNGYKVLAKRKSQDGF 60

Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLVDYNGGE 180
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLVDYNGGE 120

Qy 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240
Db 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180

Qy 241 CKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFYSQDVS 300
Db 181 CKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFYSQDVS 240

Qy 301 QMVENILHQLPQPGRTVAACDLQLLHKDQRLGSKADFLIEIKNHYFFSPINWDDL 360
Db 241 QMVENILHQLPQPGRTVAACDLQLLHKDQRLGSKADFLIEIKNHYFFSPINWDDL 300

Qy 361 YHKRLTPFPNPVNTGPDADLKHDFEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
Db 301 YHKRLTPFPNPVNTGPDADLKHDFEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360

Qy 421 DDDILDC 427
Db 361 DDDILDC 367

RESULT 8
AAU28087
ID AAU28087 standard; protein; 367 AA.

XX AAU28087;

XX 18-DEC-2001 (first entry)

XX Novel human secretory protein, Seq ID No 256.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
XX ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
XX transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
XX amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
XX ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
XX gut protection; lung; liver fibrosis; immune deficiency; infection;
XX severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
XX fertility; analgesic; pain; antigen.

XX Homo sapiens.

XX WO200166689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US0004942.

XX 07-MAR-2000; 2000US-00519705.

XX 19-MAY-2000; 2000US-00574454.

XX 17-JUN-2000; 2000US-00596193.

PR 14-JUL-2000; 2000US-00616847.
PR 19-SEP-2000; 2000US-00665363.
PR 20-OCT-2000; 2000US-00693267.
XX
XX
PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX WPI; 2001-589934/66.
DR N-PSDB; AAS44987.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis and treatment of
PT cancer, neurological, inflammatory, and autoimmune disorders.

XX Example 4; SEQ ID NO 256; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)
CC and polynucleotides (II). (I) and (II) are useful for treating
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is-
CC involved in increasing haematopoiesis, stem cell survival, bone growth
CC and remodeling. (I), (II) and modulators of (II) are useful for
CC prophylaxis or treatment of one or more cancers. (II) is also useful for
CC creating transgenic animals useful for studying the in vivo activities of
CC the polypeptide as well as for studying modulators of the polypeptides.
CC (I) induces the proliferation of neural cells and regeneration of nerve
CC and brain tissue and is useful for the treatment of central and
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis and is useful for treating myeloid
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,
CC or periodontal disease. Furthermore, (I) is also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, various immune deficiencies and
CC disorders including severe combined immunodeficiency (SCID), bacterial or
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC reactions and conditions, such as asthma or other respiratory problems.
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
CC fertility, metabolism, catabolism, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU28020-AAU28395 represent novel human secreted protein
CC amino acid sequences of the invention

XX SQ Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 6.5e-170;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 MNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVGKNGYKVLAKRKSQDGF 120
Db 1 MNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVGKNGYKVLAKRKSQDGF 60

Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLVDYNGGE 180

Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLVDYNGGE 120

Qy 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240

Db 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180

Qy 241 CKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFYSQDVS 300

Db 181 CKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFFYSQDVS 240

QY 301 QMYENILHQLOIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINKNHVFFSPINWDDL 360
Db 241 QMYENILHQLOIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINKNHVFFSPINWDDL 300
QY 361 YHKRLTPPPNPNVTGPADLKHDPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
Db 301 YHKRLTPPPNPNVTGPADLKHDPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 421 DDDILDC 427
Db 361 DDDILDC 367
RESULT 9
AAE22765
ID AAE22765 standard; protein; 367 AA.
XX
AC AAE22765;
XX
DT 09-AUG-2002 (first entry)
XX
DE Human serum and glucocorticoid-induced protein kinase, SGK2-alpha.
XX
KW Human; cytostatic; antisense gene therapy; screening; protein kinase;
KW cancer; liver; colon; tumour; inflammation; arthritic synovium; enzyme;
KW serum and glucocorticoid-induced protein kinase; SGK2-alpha.
XX
OS Homo sapiens.
XX
PN WO200224947-A2.
XX
PD 28-MAR-2002.
XX
PF 20-SEP-2001; 2001WO-IB002237.
XX
PR 20-SEP-2000; 2000US-0233999P.
PR 02-OCT-2000; 2000US-0237419P.
PR 02-OCT-2000; 2000US-0237423P.
PR 04-OCT-2000; 2000US-0238588P.
PR 10-MAY-2001; 2001US-0290555P.
XX
PA (KINE-) KINETEK PHARM INC.
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX
XX Yoganathan T; Delaney AD;
XX
XX WPI: 2002-394145/42.
DR N-PSDB; AADJ6141.
XX
XX
PT Diagnosing cancer, comprises determining the upregulation of expression
PT of a nucleic acid sequence encoding a protein kinase or upregulation of
PT expression of the protein kinase, in the cancer.
XX
XX Claim 1; Page 66-67; 87pp; English.
XX
CC The invention relates to a method for screening biologically active agent
CC that modulates cancer associated protein kinase function. The invention
CC also relates to a method for diagnosing cancer comprising determining the
CC upregulation of expression of a nucleic acid sequence encoding a protein
CC kinase. The method is useful for diagnosing cancer. A protein kinase is
CC useful for screening biological agents that modulate cancer associated
CC protein kinase function. Downregulating the activity of protein kinase is
CC useful for inhibiting the growth of a cancer cell, e.g. liver or colon
CC cancer. A nucleic acid encoding protein kinase is useful to screen biopsy
CC derived tumours and inflammatory samples such as arthritic synovium, for
CC amplified DNA in the cell or increased expression of corresponding mRNA
CC or protein, and is also useful to detect differences in expression levels
CC such as molecular weight, amino acid and nucleotide sequences between the
CC two cells. The present sequence is human serum and glucocorticoid-induced
CC protein kinase, SGK2-alpha
XX
XX Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 5; Length 367;
Best Local Similarity 100.0%; Pred. No. 6.5e-170;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFDLKVIKGNYGKVLAKRKSDGAF 120
Db 1 MNSSPAGTSPQPSRANGNINIGPSANPNAQPTDFDLKVIKGNYGKVLAKRKSDGAF 60
QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 180
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPKLYFVLDYVNGGE 120
QY 181 LFFHLQRRERFLEPRARFYAAEVAISAIGYLHLSINIYRDLKPENILLDCQGHVLTDFGL 240
Db 121 LFFHLQRRERFLEPRARFYAAEVAISAIGYLHLSINIYRDLKPENILLDCQGHVLTDFGL 180
QY 241 CKEGVEPEDTTSTFCGTPPEYLAPKPEPYDRAVDMWCLGAVLYEMLHGLPPFYSQDVS 300
Db 181 CKEGVEPEDTTSTFCGTPPEYLAPKPEPYDRAVDMWCLGAVLYEMLHGLPPFYSQDVS 240
QY 301 QMYENILHQLOIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINKNHVFFSPINWDDL 360
Db 241 QMYENILHQLOIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINKNHVFFSPINWDDL 300
QY 361 YHKRLTPPPNPNVTGPADLKHDPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
Db 301 YHKRLTPPPNPNVTGPADLKHDPDFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 421 DDDILDC 427
Db 361 DDDILDC 367
RESULT 10
ADD45799
ID ADD45799 standard; protein; 367 AA.
XX
AC ADD45799;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein XP_009494, SEQ ID NO 11468.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI: 2003-268312/26.
DR GENEANK; XP_009494.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 7; Length 367;
Best Local Similarity 100.0%; Pred. No. 6.5e-170;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 MNSSPAGTSPQPSRANGNINLGSANPNAOPTDFDLKVGKNGKVLAKRKSQDGF 120
DB 1 MNSSPAGTSPQPSRANGNINLGSANPNAOPTDFDLKVGKNGKVLAKRKSQDGF 60
QY 121 YAVKVLQKSIILKKKEQSHIMAEVSALLKNVRHPLVGLRYSFQTPPEKLYFVLDDYNGGE 180
DB 61 YAVKVLQKSIILKKKEQSHIMAEVSALLKNVRHPLVGLRYSFQTPPEKLYFVLDDYNGGE 120
QY 181 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240
DB 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
QY 241 CKEGVEPEDTSTFCGTPEYLAPEVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVDS 300
DB 181 CKEGVEPEDTSTFCGTPEYLAPEVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVDS 240
QY 301 QMYENILHQLQIPGGRTVAACDLQSLHLKQORQLGSKADFLKTNHVFSPINWDDL 360
DB 241 QMYENILHQLQIPGGRTVAACDLQSLHLKQORQLGSKADFLKTNHVFSPINWDDL 300
QY 361 YHKRLTPPPNPVNTGPAHLKHFDPPTQEAVSKSIGCTPDTVASSSGASSAFGLGFSVAPE 420
DB 301 YHKRLTPPPNPVNTGPAHLKHFDPPTQEAVSKSIGCTPDTVASSSGASSAFGLGFSVAPE 360
QY 421 DDILDC 427
DB 361 DDILDC 367

RESULT 11

ID ADI29317
AC ADI29317 standard; protein; 367 AA.
XX AC ADI29317;
XX AC ADI29317;
DT 22-APR-2004 (first entry)
XX DE Human MARK3-associated protein #87.
XX

KW Human; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorder;
KW hyperproliferative disorder; cytostatic.

OS Homo sapiens.

XX US2003232771-A1.

XX 18-DEC-2003.

XX 17-JUN-2002; 2002US-00174319.

XX 17-JUN-2002; 2002US-00174319.

PA (ISIS-) ISIS PHARM INC.

PI Ward DT, Freier SM, Dobie KW;

XX WPI; 2004-052188/05.

DR N-PSDB; ADI29435.

XX New antisense compound targeted to a nucleic acid molecule encoding
PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
PT expression of MARK3 or for treating cancer or Alzheimer's disease.

XX Disclosure; SEQ ID NO 237; 233pp; English.

XX The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding MARK3
CC (MAP/microtubule affinity-regulating kinase 3), that specifically
CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression
CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
CC composition comprising the compound and a carrier or diluent, inhibiting or
CC the expression of MARK3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with MARK3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer and neurodegenerative diseases e.g.
CC Alzheimer's disease. The present sequence is a MARK3 associated protein
CC included in the figures but not mentioned anywhere else in the
CC specification.

XX SQ Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 8; Length 367;
Best Local Similarity 100.0%; Pred. No. 6.5e-170;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 MNSSPAGTSPQPSRANGNINLGSANPNAOPTDFDLKVGKNGKVLAKRKSQDGF 120
DB 1 MNSSPAGTSPQPSRANGNINLGSANPNAOPTDFDLKVGKNGKVLAKRKSQDGF 60
QY 121 YAVKVLQKSIILKKKEQSHIMAEVSALLKNVRHPLVGLRYSFQTPPEKLYFVLDDYNGGE 180
DB 61 YAVKVLQKSIILKKKEQSHIMAEVSALLKNVRHPLVGLRYSFQTPPEKLYFVLDDYNGGE 120
QY 181 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240
DB 121 LFFHLQRRERFLPRARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180
QY 241 CKEGVEPEDTSTFCGTPEYLAPEVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVDS 300
DB 181 CKEGVEPEDTSTFCGTPEYLAPEVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVDS 240
QY 301 QMYENILHQLQIPGGRTVAACDLQSLHLKQORQLGSKADFLKTNHVFSPINWDDL 360
DB 241 QMYENILHQLQIPGGRTVAACDLQSLHLKQORQLGSKADFLKTNHVFSPINWDDL 300
QY 361 YHKRLTPPPNPVNTGPAHLKHFDPPTQEAVSKSIGCTPDTVASSSGASSAFGLGFSVAPE 420
DB 301 YHKRLTPPPNPVNTGPAHLKHFDPPTQEAVSKSIGCTPDTVASSSGASSAFGLGFSVAPE 360

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QY 421 DDILDC 427
Db 361 DDILDC 367

RESULT 12
ADJ45521
ID ADJ45521 standard; protein; 367 AA.
XX AC
AC ADJ45521;
DT 06-MAY-2004 (first entry)
XX DE
DE LXR-ligand induced transcript seq id 52.
XX KW
KW LXR; liver X receptor; cholesterol; gallstone; atherosclerosis;
KW lipid storage disease; obesity; diabetes; hypercholesterolaemia;
KW LXR-ligand induced 1; LXRL1; human; LXR-ligand induced transcript;
KW LXR regulated gene.
XX OS
OS Homo sapiens.
XX PN
PN US2004023276-A1.
XX PD
PD 05-FEB-2004.
XX PF
PF 02-MAY-2003; 2003US-00429160.
XX PR
PR 03-MAY-2002; 2002US-037714P.
XX PA
PA (WARD/) WARD T R.
PA (MAOM/) MAO M.
PA (LINS/) LINSLEY P S.
PA (LUND/) LUND E.
XX PI
PI Ward TR, Mao M, Linsley PS, Lund E;
XX DR
DR WPI; 2004-224687/21.
DR N-PSDB; ADJ45520.
XX PT
PT New purified Liver X receptor (LXR) nucleic acids, useful for diagnosing
PT a disease involving LXR activity, such as cholesterol gallstones,
PT atherosclerosis, lipid storage diseases, obesity, diabetes, or
PT hypercholesterolemia.
XX PS
PS Example 1; SEQ ID NO 52; 141pp; English.
XX CC
CC The invention describes a purified nucleic acid comprising a fully
CC defined sequence of 1586 bp (SEQ ID NO: 1) as given in the specification,
CC or its complement. The methods and compositions are useful for diagnosing
CC a disease or disorder involving LXR (liver X receptor) activity in a
CC sample by detecting an increase or decrease in the transcript level
CC relative to the amount present in an analogous sample from a subject not
CC having the disease or disorder or not subjected to therapy, wherein the
CC disease or disorder is cholesterol gallstones, atherosclerosis, lipid
CC storage diseases, obesity, diabetes, or hypercholesterolemia. They are
CC also used to identify a compound that changes LXR activity, wherein the
CC compound changes the estimated level of LXR activity in a sample from the
CC subject contacted with the compound relative to the estimated level of
CC LXR activity in an analogous sample from the subject not contacted with
CC the compound. This is the amino acid sequence of an LXR regulated
CC protein.
XX SQ
SQ Sequence 367 AA;

Query Match 84.6%; Score 1954; DB 8; Length 367;
Best Local Similarity 100.0%; Pred. No. 6.5e-170;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYKVLAKRKSDGAF 120
Db 1 MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYKVLAKRKSDGAF 60

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QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLQVNGGE 180
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLQVNGGE 120

QY 181 LFFHLQRRRRFLEPRARFYAAEVASAIQYLHLSNIIYRDLKPENILLDCQGHVVLTFDGL 240
Db 121 LFFHLQRRRRFLEPRARFYAAEVASAIQYLHLSNIIYRDLKPENILLDCQGHVVLTFDGL 180

QY 241 CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVVS 300
Db 181 CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDVVS 240

QY 301 QMVENILHQPLOIPGGRVTAAACDLQSLHKKORQLGSKADPELEIKNVHFFSPINWDDL 360
Db 241 QMVENILHQPLOIPGGRVTAAACDLQSLHKKORQLGSKADPELEIKNVHFFSPINWDDL 300

QY 361 YHKRLTTPPNPNVTGPDALKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
Db 301 YHKRLTTPPNPNVTGPDALKHFDPEFTQBAVSKSIGCTPDTVASSSGASSAFLGFSYAPE 360

QY 421 DDILDC 427
Db 361 DDILDC 367

RESULT 13
AAB65708
ID AAB65708 standard; protein; 367 AA.
XX AC
AC AAB65708;
XX DT
DT 27-MAR-2001 (first entry)
XX DE
DE Novel protein kinase, SEQ ID NO: 237.
XX KW
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX OS
OS Homo sapiens.
XX PN
PN WO200073469-A2.
XX PD
PD 07-DEC-2000.
XX PF
PF 26-MAY-2000; 2000WO-US014842.
XX PR
PR 28-MAY-1999; 99US-0136503P.
XX PA
PA (SUGE-) SUGEN INC.
XX PI
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX DR
DR WPI; 2001-032161/04.
DR N-PSDB; AAF44737.
XX PT
PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
XX PS
PS Claim 10; Fig 1; 310pp; English.
XX CC
CC The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies

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CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders

XX Sequence 367 AA;

Query Match 84.5%; Score 1952; DB 4; Length 367;

Best Local Similarity 99.7%; Pred. No. 9.9e-170;

Matches 366; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 61 MNSSPACTPSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKKSDGAF 120
DB 1 MNSSPACTPSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKKSDGAF 60

QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYVNGE 180

DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYVNGE 120

QY 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTFDGL 240

DB 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTFDGL 180

QY 241 CKGEVPEPDTTSTFCGTPEYLAPEVLKKEPYDRAVWVCLGAVLYEMLHGLPPYSQDVS 300

DB 181 CKGEVPEPDTTSTFCGTPEYLAPEVLKKEPYDRAVWVCLGAVLYEMLHGLPPYSQDVS 240

QY 301 QMYENILHQPLOIPGGRITVAACDLQSLHKKQRLGSKADFLKIKNHVFFSPINWDDL 360

DB 241 QMYENILHQPLOIPGGRITVAACDLQSLHKKQRLGSKADFLKIKNHVFFSPINWDDL 300

QY 361 YHKELTPFPNPNVTGPADLKHDFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFLGFSYAPE 420

DB 301 YHKELTPFPNPNVTGPADLKHDFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFLGFSYAPE 360

QY 421 DDIDLDC 427

DB 361 DDIDLDC 367

RESULT 14

AA95277

ID AA95277 standard; protein; 367 AA.

XX

AC AA95277;

XX

DT 12-SEP-2000 (first entry)

XX

DE Mouse serum and glucocorticoid-induced protein kinase 2.

XX

XX Serum and glucocorticoid-induced protein kinase 2; SGK2; mouse;

XX phosphorylation; cancer; diabetes; ischaemia; therapy.

XX

OS Mus musculus.

XX

FN WO200035946-A1.

XX

PD 22-JUN-2000.

XX

PF 14-DEC-1999; 99WO-GB004232.

XX

PR 14-DEC-1998; 98US-0112217P.

XX

PR 19-AUG-1999; 99GB-00019676.

XX

PA (UYDU-) UNIV DUNDEE.

XX

XX Cohen P, Kobayashi T, Deak M;

PI

DR WPI; 2000-442364/38.

XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)
PT or dephosphorylation, useful for treatment of cancer, diabetes and
PT ischaemic diseases.

XX Disclosure; Page 7; 127pp; English.

XX The present sequence is that of mouse serum and glucocorticoid-induced
CC protein kinase (SGK) isoform 2, a protein activated by phosphorylation.
CC The invention provides methods of activating SGK (see also AAY95275-79)
CC by phosphorylation using 3-phosphoinositide-dependent protein kinase-1
CC (PDK1), and of reducing the activity of SGK by dephosphorylation. The
CC invention also provides a method of identifying a compound that modulates
CC the activity of SGK. Such compounds are useful for treating patients
CC requiring modulation of SGK, such as patients with cancer, diabetes or
CC ischaemic disease

XX Sequence 367 AA;

Query Match 80.0%; Score 1848; DB 3; Length 367;

Best Local Similarity 94.3%; Pred. No. 3.3e-160;

Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 61 MNSSPACTPSPQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKKSDGAF 120

DB 1 MASSPVGVPSQPSRANGNINLGPSANPNAQPTDFDLKVGKNGYGVLLAKKSDGAF 60

QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYVNGE 180

DB 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDYVNGE 120

QY 181 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTFDGL 240

DB 121 LFFHLQRRERFLEPRARFYAAEVAASAIYGLHSLNIIYRDLKPENILLDCQGHVVLTFDGL 180

QY 241 CKGEVPEPDTTSTFCGTPEYLAPEVLKKEPYDRAVWVCLGAVLYEMLHGLPPYSQDVS 300

DB 181 CKGEVPEPDTTSTFCGTPEYLAPEVLKKEPYDRAVWVCLGAVLYEMLHGLPPFTDVA 240

QY 301 QMYENILHQPLOIPGGRITVAACDLQSLHKKQRLGSKADFLKIKNHVFFSPINWDDL 360

DB 241 QMYENILHQPLOIPGGRITVAACDLQSLHKKQRLGSKADFLKIKNHVFFSPINWDDL 300

QY 361 YHKELTPFPNPNVTGPADLKHDFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFLGFSYAPE 420

DB 301 YHKELTPFPNPNVTGPADLKHDFDPEFTQEAIVSKSIGCTPTDVASSSGASSAFLGFSYAQD 360

QY 421 DDIDLDC 426

DB 361 DDIDLDC 366

RESULT 15

ADD45797

ID ADD45797 standard; protein; 367 AA.

XX

AC ADD45797;

XX

DT 29-JAN-2004 (first entry)

XX

DE Rat Protein AAF12756, SEQ ID NO 11466.

XX

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

OS

XX WO2003016475-A2.

PN

XX 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; AAF12756.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 367 AA;

Query Match 80.0%; Score 1848; DB 7; Length 367;
Best Local Similarity 94.3%; Pred. No. 3.3e-160;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 61 MNSSPAGTPSPQPSRANGNINLGSANPNAPQTDDEFLKVIGKNGYKVLAKRKS DGAF 120
Db 1 MASSPGVSPQPSRANGNINLGSANPNARPTDEFLKVIGKNGYKVLAKRKS DGAF 60
QY 121 YAVKVLQKKSILKKQESHIMAEERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 180
Db 61 YAVKVLQKKSILKNKQNHIMAEERNVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 120
QY 181 LFFHLQRRERFLPRARFYAAEVASAIYGLHSNIIYRDLKPNENILLDCQGHVLTDFGL 240
Db 121 LFFHLQRRERFLPRARFYTAEVASAIYGLHSNIIYRDLKPNENILLDCQGHVLTDFGL 180
QY 241 CKEGVEPDDTTSTFCGTPPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFYSDVS 300
Db 181 CKECVPEETSTSTFCGTPPEYLAPEVLKPEYDRAVDWCLGAVLYEMLHGLPPFFNTDVA 240
QY 301 QMYENILHQLQIPGGRTVAACDLQSLHKKDQRQLGSKADFEIKNHVFFSPINWDDL 360
Db 241 QMYENILHQLQIPGGRTVAACDLQGLLHKDQRQLGSKEDFLDIKNHMFSPINWDDL 300

QY 361 YHKRLTPPENPNVTGPADLKHFDPERTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
Db 301 YHKRLTPPENPNVNEGPA DLKHFDPERTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAO D 360
QY 421 DDDILD 426
Db 361 DDDILD 366

Search completed: January 27, 2006, 23:26:44
Job time : 79.0006 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2006, 23:21:11 ; Search time 20.1415 Seconds
(without alignments)
1752.724 Million cell updates/sec

Title: US-09-868-131A-8

Perfect score: 2311

Sequence: 1 MQGLLTSGRKPSGGGRCTGR.....ASSAFLGFSYAPEDDDILDLC 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1419	61.4	407	2	US-10-067-977-4
2	1419	61.4	445	2	US-10-067-977-2
3	1415	61.2	431	2	US-09-031-295-2
4	1415	61.2	431	2	US-10-000-039-2
5	1411.5	61.1	430	1	US-08-712-709-9
6	1411.5	61.1	430	2	US-09-111-444-9
7	1411.5	61.1	430	2	US-09-541-228-9
8	1411	61.1	431	1	US-08-712-709-5
9	1411	61.1	431	2	US-09-111-444-5
10	1411	61.1	431	2	US-09-541-228-5
11	891	38.6	479	2	US-09-771-161A-246
12	891	38.6	479	2	US-09-771-161A-247
13	891	38.6	479	2	US-09-771-161A-248
14	883.5	38.2	465	2	US-09-526-043-2
15	882.5	38.2	454	2	US-09-526-043-17
16	878.5	38.0	480	2	US-09-590-740-6
17	876	37.9	480	2	US-09-526-043-13
18	876	37.9	481	2	US-09-538-092-1054
19	874.5	37.8	480	2	US-09-091-058-2
20	874.5	37.8	480	2	US-09-590-740-2
21	874.5	37.8	480	2	US-09-538-092-1053
22	874.5	37.8	480	2	US-09-526-043-14
23	874.5	37.8	480	2	US-09-771-161A-223
24	874.5	37.8	726	2	US-09-417-197-71
25	874.5	37.8	727	2	US-09-417-197-139
26	856	37.0	417	2	US-09-590-740-4
27	849.5	36.8	480	2	US-09-205-658-157

28	844.5	36.5	470	2	US-09-248-796A-18482	Sequence 18482, A
29	801	34.7	637	2	US-09-817-310-2	Sequence 2, Appli
30	801	34.7	637	2	US-10-355-724A-2	Sequence 2, Appli
31	799.5	34.6	587	1	US-08-313-274-2	Sequence 2, Appli
32	799.5	34.6	655	2	US-09-949-016-11676	Sequence 11676, A
33	788.5	34.1	482	2	US-09-430-564-2	Sequence 2, Appli
34	788.5	34.1	495	2	US-09-430-564-3	Sequence 3, Appli
35	788.5	34.1	495	2	US-09-762-258-2	Sequence 2, Appli
36	788	34.1	546	2	US-09-205-658-155	Sequence 155, App
37	783.5	33.9	541	2	US-09-205-658-154	Sequence 154, App
38	782.5	33.9	502	2	US-09-538-092-996	Sequence 996, App
39	782.5	33.9	525	1	US-08-749-902-7	Sequence 7, Appli
40	782.5	33.9	525	1	US-08-749-902-8	Sequence 8, Appli
41	782.5	33.9	525	2	US-09-430-564-16	Sequence 16, Appli
42	782.5	33.9	525	2	US-09-762-258-4	Sequence 4, Appli
43	770	33.3	737	2	US-09-772-647-4	Sequence 4, Appli
44	770	33.3	737	2	US-10-328-931-4	Sequence 4, Appli
45	769	33.3	568	2	US-09-949-016-7970	Sequence 7970, Ap

ALIGNMENTS

RESULT 1

US-10-067-977-4

; Sequence 4, Application US/10067977

; Patent No. 6830911

; GENERAL INFORMATION:

; APPLICANT: YAN, Chunhua and KE, Zhaoxi

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CL001313

; CURRENT APPLICATION NUMBER: US/10/067,977

; CURRENT FILING DATE: 2002-02-08

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 407

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-067-977-4

Query Match 61.4%; Score 1419; DB 2; Length 407;
Best Local Similarity 68.3%; Pred. No. 5.3e-125;
Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

Qy	38	PTPTTLLSCLLPVPPPELPHCYRMSSPAGTPSPQPSRANGTNLGPANPNAPQPTDFD	97
Db	28	PEVQSILKISQPEPEL-----MNAHP--SPPPSPSQ---QINLGSSNPHAKPSDFH	76
Qy	98	LKVIKGNVGVLLAKKSGDGFYAVKVLQKSKILKKQSHIMAEVSLLKNVRHPLV	157
Db	77	LKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIMSERNVLLKNVHPLV	136
Qy	158	GLRYSFQTEPKLFYLDVYNGGSLFFHLQREERFLPRPFYAAEVASAIYLHSLNIY	217
Db	137	GLHFSFQTDKLVFDVLYNGGELFHLQRECFLEPRPFYAAETASALYHLSNIY	196
Qy	218	RLDKPENILLDCQGHVLTDFGLCKEGVPEPTTSTFCGTPPEYLAPEVLKPEYDRAVDW	277
Db	197	RLDKPENILLDSQGHVLTDFGLCKENIHNSTTSTFCGTPPEYLAPEVLKPYDRTVDW	256
Qy	278	WCLGAVLYEMHLGHPFFYSQDVSMYENILHQLQIPGGRTVAACDLQLSLHKDQRL	337
Db	257	WCLGAVLYEMLYGLPPFFYSRNTAEYDNLINKLQKLPKNTNSARHLLEGLQDKTKRL	316
Qy	338	GSKADFLKTNHVFSPINWDDLYHKRLTPPNPNVTGPADLKHDFPEFTQEAVSKSIGC	397
Db	317	GAKDFMEIKSHVFFSLINWDDLLINKKITPPFPNPNVSGPNDLRHDFPEFTPEEPVNSIGK	376
Qy	398	TPDVT---ASSGASSAFLGFSYAPEDDDIL 425	

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Db 377 SPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 407

RESULT 2
US-10-067-977-2
; Sequence 2, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-977-2

Query Match 61.4%; Score 1419; DB 2; Length 445;
Best Local Similarity 68.3%; Pred. No. 6.1e-125;
Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 38 PPTPTLSCLLLVPPELPDHCYMNSSPAGTSPQPSRANGNINLGPSANPNNAQPTDFDF 97
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
66 PEVQSILKISQOEPEL-----MNAHP--SPPPSPSQ---QINLGFSSNPHAKPSDFHF 114
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

QY 98 LKVIKGNKYKVLAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPELV 157
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
115 LKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIMSERVLLKNVHPELV 174
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

QY 158 GLRYSQTPEKLYFVLDYVNGGELFPHLQRRERFLEPRARFYAAEVAASAIYHLSNIIV 217
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
175 GLHFSQTADKLYFVLDYINGGELFYHLQRCFLEPRARFYAAETASALYHLSNIIV 234
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

QY 218 RDLKPENILLDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDW 277
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
235 RDLKPENILLDSQGHVLTDFGLCKENIEHNS'TSTFCGTPEYLAPEVLHKKPYDRTVDW 294
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

QY 278 WCLGAVLYEMLHGLPPFYSDQVSYQMYENILHQPLOIPGGRTVAACDLQSLHKKQORQL 337
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
295 WCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSARHLLGGLQKDRTKRL 354
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

QY 338 GSKADPLEIKNHFVFFSPINWDDLYHKRLTPFPNPNVTGPDADLKHPDPEFTQEAIVKSIGC 397
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
355 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLHDFDPEETEEFPVPSIGK 414
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

QY 398 TPDTV---ASSSGASAFGLGFSYAPEDDIL 425
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
415 SPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 445
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 3
US-09-031-295-2
; Sequence 2, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
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; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,444
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 294637
;
US-09-111-444-9

Query Match 61.1%; Score 1411.5; DB 2; Length 430;
Best Local Similarity 69.7%; Pred. No. 2.9e-124;
Matches 265; Conservative 56; Mismatches 44; Indels 15; Gaps 5;

QY 49 PVPELPDHCYRMNSSPAGTSPQPSRANGINLGPSANPNAPTDFDLKLVIGKGYGK 108
DB 63 PQPEL-----NNANP--SPPSPSQ---QINLGFSSNPHAKPSDFHLKVGKSGFK 111
QY 109 VLLAKRSGDAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKEK 168
DB 112 VLLARHKAEAFYAVKVLQKKAIIKKKEKHIMSERNVLLKNVKHPFLVGLHPSFQTADK 171
QY 169 LFFVLVDYNGGELFFHLQRRERFLPRARFYAAEASATGYLHSLNIIVRDLPENILLD 228
DB 172 LYFVLVDYINGGELFFHLQRRERFLPRARFYAAEASATGYLHSLNIIVRDLPENILLD 231
QY 229 CQGHVVLTPDFGLCKEGVEPEDTSTFCGTPPEYLAPPEVLKPEYDRAVDWMLGAVLYEML 288
DB 232 SQGHIVLTDFGLCKENIEHNGTTSTFCGTPPEYLAPPEVLKQPDVDRVDMWCLGAVLYEML 291
QY 289 HGLPPFPYSQDVSMYENILHQPFIQPGRTVAACDLQLSLHKDQRLGSKADFLFIKN 348
DB 292 YGLPPFPYSRNTAEYDNIILNKPQLK-NITNSARHLEGLLQKDKRTKRLGAKDDFWEIKS 350
QY 349 HVFPSPINWDDLHYKRLTPFPNPNVTPGADLKHFDFEFTQEAIVSKIGCTPDTV---ASS 405
DB 351 HIFPFLINWDDLINKKITPFPNPNVSGPSDLRHFDPFTEEPVPSIGRSPDSILVTASV 410
QY 406 SGASSAFLGFSYAPEDDDIL 425
; : ||||| | | |
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DB 411 KEAAEAFGLGFSYAPMDSFL 430

RESULT 7
US-09-541-228-9
; Sequence 9, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 294637
;
US-09-541-228-9

Query Match 61.1%; Score 1411.5; DB 2; Length 430;
Best Local Similarity 69.7%; Pred. No. 2.9e-124;
Matches 265; Conservative 56; Mismatches 44; Indels 15; Gaps 5;

QY 49 PVPELPDHCYRMNSSPAGTSPQPSRANGINLGPSANPNAPTDFDLKLVIGKGYGK 108
DB 63 PQPEL-----NNANP--SPPSPSQ---QINLGFSSNPHAKPSDFHLKVGKSGFK 111
QY 109 VLLAKRSGDAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKEK 168
DB 112 VLLARHKAEAFYAVKVLQKKAIIKKKEKHIMSERNVLLKNVKHPFLVGLHPSFQTADK 171
QY 169 LFFVLVDYNGGELFFHLQRRERFLPRARFYAAEASATGYLHSLNIIVRDLPENILLD 228
DB 172 LYFVLVDYINGGELFFHLQRRERFLPRARFYAAEASATGYLHSLNIIVRDLPENILLD 231
QY 229 CQGHVVLTPDFGLCKEGVEPEDTSTFCGTPPEYLAPPEVLKPEYDRAVDWMLGAVLYEML 288
DB 232 SQGHIVLTDFGLCKENIEHNGTTSTFCGTPPEYLAPPEVLKQPDVDRVDMWCLGAVLYEML 291
QY 289 HGLPPFPYSQDVSMYENILHQPFIQPGRTVAACDLQLSLHKDQRLGSKADFLFIKN 348
DB 292 YGLPPFPYSRNTAEYDNIILNKPQLK-NITNSARHLEGLLQKDKRTKRLGAKDDFWEIKS 350
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QY 158 GLRYSQTPEKLYFVLDYVNGGELFPHLQRRERFLEPRARFYAAEVASAIYGLHSLNIY 217
DB 161 GLHFSQTADKLYFVLDYVNGGELFPHLQRRERFLEPRARFYAAEVASAIYGLHSLNIY 220
QY 218 RDLKPENILLDCOGHVLTDFGLCKEGVEPEDTSTFCGTPEYLAPEVLKRPYDRAVDW 277
DB 221 RDLKPENILLDSQGHVLTDFGLCKENIEHNSTSTFCGTPEYLAPEVLKRPYDRTVDW 280
QY 278 WCLGAVLYEMLHGLPPFYSDVSMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORQL 337
DB 281 WCLGAVLYEMLYGLPPFYSRNTAEYDNLINKPLQKPNITNSARHLLGGLQKDRTKRL 340
QY 338 GSKADPLEIKNHVFFSPINWDDLKHRLTPPNPNVTGPADLKHFPDPTQEAIVSKSICG 397
DB 341 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLRHFDPEETEEVPNSIGK 400
QY 398 TPDTV---ASSGASSAFGLFSYAPEDDDIL 425
DB 401 SPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 10

US-09-541-228-5
; Sequence 5, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-09-541-228-5

Query Match 61.1%; Score 1411; DB 2; Length 431;
Best Local Similarity 68.0%; Pred. No. 3.3e-124;
Matches 266; Conservative 56; Mismatches 55; Indels 14; Gaps 4;
QY 38 PPTPTLSCLLLPVPELPDPHCYRMNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDF 97

DB 52 PEVQSILKISQOEPEL-----MNAHP--SPPPSPQ---QINLGPSSNPHAKPSDFHF 100
QY 98 LKVIKGNKYGVLLAKRRSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLV 157
DB 101 LKVIKGSFGVLLARHKAEEVFYAVKVLQKAILKKKEKHIMSERVLLKNVHPFLV 160
QY 158 GLRYSQTPEKLYFVLDYVNGGELFPHLQRRERFLEPRARFYAAEVASAIYGLHSLNIY 217
DB 161 GLHFSQTADKLYFVLDYVNGGELFPHLQRRERFLEPRARFYAAEVASAIYGLHSLNIY 220
QY 218 RDLKPENILLDCOGHVLTDFGLCKEGVEPEDTSTFCGTPEYLAPEVLKRPYDRAVDW 277
DB 221 RDLKPENILLDSQGHVLTDFGLCKENIEHNSTSTFCGTPEYLAPEVLKRPYDRTVDW 280
QY 278 WCLGAVLYEMLHGLPPFYSDVSMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORQL 337
DB 281 WCLGAVLYEMLYGLPPFYSRNTAEYDNLINKPLQKPNITNSARHLLGGLQKDRTKRL 340
QY 338 GSKADPLEIKNHVFFSPINWDDLKHRLTPPNPNVTGPADLKHFPDPTQEAIVSKSICG 397
DB 341 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLRHFDPEETEEVPNSIGK 400
QY 398 TPDTV---ASSGASSAFGLFSYAPEDDDIL 425
DB 401 SPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 11

US-09-771-161A-246
; Sequence 246, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 246
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-246

Query Match 38.6%; Score 891; DB 2; Length 479;
Best Local Similarity 48.5%; Pred. No. 3.4e-75;
Matches 182; Conservative 55; Mismatches 100; Indels 38; Gaps 8;
QY 60 RMNSSPAGTSPQPSRAN--GNINLGPSANPNAQPT--DFDLKIVTGGKNGYGVLLAKRK 115
DB 116 RMNCSPT-----SQIDNIGEEEMDASTTHHKRKTMDFDYLLKLGKGTGKGVILVREK 168
QY 116 SDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDY 175
DB 169 ASGKYAMKILKKEVIIAKDEVAHTLUTE--SRVLKNTRHPPFLTSLKYSFQTKRLCFVMEY 227
QY 176 VNGGELFPHLQRRERFLEPRARFYAAEVASAIYGLHSLNIYRDLKPENILLDCQGHVVL 235
DB 228 VNGGELFPHLSRERFSEDRTRYGAEIVSALDYLSHGKIVYRDLKLENLMDKDGHIKI 287
QY 236 TDFGLCKEGVEPEDTSTFCGTPEYLAPEVLKRPYDRAVDWVCLGAVLYEMLHGLPPFY 295
DB 288 TDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDNDYGRAVDWMGLGVWVYEMMCGRLPFY 347
QY 296 SDVSMYENILHQPLOIPGGRTVAACDLLOSLLHKDQORQL--GSKADPLEIKNHVFFSP 354

Db 348 NQDEKLFELIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRKLGCGPDDAKEIMRHSFFSG 407
QY 355 INWDDLYHKRLTPFPNPNVTGPADLKHFDPFTEQEAUVSKSGCTPDTVASSSGASSAFLG 414
Db 408 VNMQDVYDKKLVLPFPKQVTSSETDTRYFDEEFT-----AQTTITTP----- 448
QY 415 FSYAPE--DDILDC 427
Db 449 ----PEKYDEGDMDC 459

RESULT 12

US-09-771-161A-247
; Sequence 247, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 247
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-247

Query Match 38.6%; Score 891; DB 2; Length 479;
Best Local Similarity 48.5%; Pred. No. 3.4e-75;
Matches 182; Conservative 55; Mismatches 100; Indels 38; Gaps 8;
QY 60 RMNSSPAGTSPQPSRAN--GNINLGPSANPNQAQPT--DFDFLKVKVIGKNGYKVLAKRK 115
Db 116 RMNCSTP-----SQIDNIGEEEMDASTTHHKRTMNDPDKLKGKGTGKGVILVREK 168
QY 116 SDGAFYAVKVLQKKSILKKKEQSHIMAEKSVLLKNVHRHPLVGLRYSFQTPKLYFVLDY 175
Db 169 ASKYYAMKILKKEVIAKDEVAHTLTE-SRVLKNTKTRHPPLTSLKYSFQTKDRLCFVMEY 227
QY 176 VNGGELFFHLQRRERFLEPRARYAAEVAASAIYGLHSLNIYYRDLKPENILLDCQGHVVL 235
Db 228 VNGGELFFHLRSRVFSEDRTRYGAEIVSALDYLSHGKIVYRDLKLENMLDKDGHKI 287
QY 236 TDFGLCKEGVEPEDTSTTCGTPPEYLAPEVLRKEPYDRAVDWMLGAVLYEMLHGLPPFY 295
Db 288 TDFGLCKEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDWMLGAVLYEMMCGRLPFY 347
QY 296 SQDVSMYENILHQLIPGGRVVAACDLLOSLLHKDQORL-GSKADFLKIKNHVFFSP 354
Db 348 NQDEKLFELIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRKLGCGPDDAKEIMRHSFFSG 407
QY 355 INWDDLYHKRLTPFPNPNVTGPADLKHFDPFTEQEAUVSKSGCTPDTVASSSGASSAFLG 414
Db 408 VNMQDVYDKKLVLPFPKQVTSSETDTRYFDEEFT-----AQTTITTP----- 448
QY 415 FSYAPE--DDILDC 427
Db 449 ----PEKYDEGDMDC 459

RESULT 13

US-09-771-161A-248
; Sequence 248, Application US/09771161A
; Patent No. 6936450

; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 248
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-248

Query Match 38.6%; Score 891; DB 2; Length 479;
Best Local Similarity 48.5%; Pred. No. 3.4e-75;
Matches 182; Conservative 55; Mismatches 100; Indels 38; Gaps 8;
QY 60 RMNSSPAGTSPQPSRAN--GNINLGPSANPNQAQPT--DFDFLKVKVIGKNGYKVLAKRK 115
Db 116 RMNCSTP-----SQIDNIGEEEMDASTTHHKRTMNDPDKLKGKGTGKGVILVREK 168
QY 116 SDGAFYAVKVLQKKSILKKKEQSHIMAEKSVLLKNVHRHPLVGLRYSFQTPKLYFVLDY 175
Db 169 ASKYYAMKILKKEVIAKDEVAHTLTE-SRVLKNTKTRHPPLTSLKYSFQTKDRLCFVMEY 227
QY 176 VNGGELFFHLQRRERFLEPRARYAAEVAASAIYGLHSLNIYYRDLKPENILLDCQGHVVL 235
Db 228 VNGGELFFHLRSRVFSEDRTRYGAEIVSALDYLSHGKIVYRDLKLENMLDKDGHKI 287
QY 236 TDFGLCKEGVEPEDTSTTCGTPPEYLAPEVLRKEPYDRAVDWMLGAVLYEMLHGLPPFY 295
Db 288 TDFGLCKEGITDAATKTKTCGTPPEYLAPEVLENDYGRAVDWMLGAVLYEMMCGRLPFY 347
QY 296 SQDVSMYENILHQLIPGGRVVAACDLLOSLLHKDQORL-GSKADFLKIKNHVFFSP 354
Db 348 NQDEKLFELIMEDIKPPRTLSDDAKSLLSGLLIKDPNKRKLGCGPDDAKEIMRHSFFSG 407
QY 355 INWDDLYHKRLTPFPNPNVTGPADLKHFDPFTEQEAUVSKSGCTPDTVASSSGASSAFLG 414
Db 408 VNMQDVYDKKLVLPFPKQVTSSETDTRYFDEEFT-----AQTTITTP----- 448
QY 415 FSYAPE--DDILDC 427
Db 449 ----PEKYDEGDMDC 459

RESULT 14

US-09-526-043-2
; Sequence 2, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 465
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-526-043-2

Query Match      38.2%; Score 883.5; DB 2; Length 465;
Best Local Similarity 51.2%; Pred. No. 1.7e-74;
Matches 173; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

QY 60 RMNSSPAGTSPQPSRAN--GNNLGFSPANPNAOPT--DPDFLKVIKGNGYKVLAKRK 115
Db 116 RMNCSPT-----SQIDNIGSEMDASTTHHKRTKTMNDFDYLKLLGKGTFGKVIILVREK 168
QY 116 SDGAFYAVKVLQKSKILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPPEKLYFVLDY 175
Db 169 ASKYYAMKLLKEVIAKDEVAHTLTS- SRVUKNTRHPPLTSLSKYSFQTKDRLCFMVEY 227
QY 176 VNGGELFFHLQRRERFLEPRARYAAEVAASGYLHSLNIIYRDLPENILLDCQGHVVL 235
Db 228 VNGGELFFHLRSRERFSEDRTRFYGAIEVSALDYLSHGKIVYRDYLDKLENLMLDKDGHKI 287
QY 236 TDFGLCKEGVEPEDTSTFCGTPPEYLAPVLRKEPYDRAVDWMCGLGAVLYEMLHGLPPFY 295
Db 288 TDFGLCKEGITDAATWKTFPGTPEYLAPVLENDYGRAVDWMCGLGVVMYEMMCGRLPPY 347
QY 296 SQDVSMQYENILHQPILQIPGGRVAAACDLQLSLHKKDQORL--GSKADFLKIKNHVFFSP 354
Db 348 NQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLLGGGPDPAKEIMRHSFFSG 407
QY 355 INWDDLYHKRLTPPPNPNTGADLKHDFPFTQEAVS 392
Db 408 VNWQDVYDKLVPPFKPQVTSSETDTRYFDEEFTAQIT 445
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Search completed: January 27, 2006, 23:33:32
Job time : 21.1415 secs

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RESULT 15
US-09-526-043-17
; Sequence 17, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-526-043-17

Query Match      38.2%; Score 882.5; DB 2; Length 454;
Best Local Similarity 51.2%; Pred. No. 2e-74;
Matches 173; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

QY 60 RMNSSPAGTSPQPSRAN--GNNLGFSPANPNAOPT--DPDFLKVIKGNGYKVLAKRK 115
Db 116 RMNCSPT-----SQIDNIGSEMDASTTHHKRTKTMNDFDYLKLLGKGTFGKVIILVREK 168
QY 116 SDGAFYAVKVLQKSKILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPPEKLYFVLDY 175
Db 169 ASKYYAMKLLKEVIAKDEVAHTLTS- SRVUKNTRHPPLTSLSKYSFQTKDRLCFMVEY 227
QY 176 VNGGELFFHLQRRERFLEPRARYAAEVAASGYLHSLNIIYRDLPENILLDCQGHVVL 235
Db 228 VNGGELFFHLRSRERFSEDRTRFYGAIEVSALDYLSHGKIVYRDYLDKLENLMLDKDGHKI 287
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
2381.178 Million cell updates/sec

Title: US-09-868-131A-8
Perfect score: 2311
Sequence: 1 MQGLLSGRKPSGGRTGR.....ASSAFLGFSYAPDDDDILDC 427

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
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6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2311	100.0	427	US-10-753-267-126	Sequence 126, App
2	2124.5	91.9	398	US-10-262-511-140	Sequence 140, App
3	2005	86.8	382	US-10-296-115-1109	Sequence 1109, App
4	2005	86.8	396	US-10-926-543-83	Sequence 83, Appl
5	1954	84.6	367	US-09-971-118-2	Sequence 2, Appl
6	1954	84.6	367	US-10-291-172-256	Sequence 256, App
7	1954	84.6	367	US-10-429-160-52	Sequence 52, Appl
8	1954	84.6	367	US-10-221-278-256	Sequence 256, App
9	1954	84.6	367	US-10-380-235-6	Sequence 6, Appl
10	1421.5	61.5	388	US-10-131-410-104	Sequence 104, App
11	1419	61.4	407	US-10-067-977-4	Sequence 4, Appl
12	1419	61.4	407	US-10-827-272-4	Sequence 4, Appl
13	1419	61.4	431	US-09-981-353-7	Sequence 7, Appl
14	1419	61.4	431	US-10-403-161-2	Sequence 2, Appl
15	1419	61.4	431	US-10-403-161-4	Sequence 4, Appl
16	1419	61.4	445	US-10-067-977-2	Sequence 2, Appl
17	1419	61.4	445	US-10-827-272-2	Sequence 2, Appl
18	1419	61.4	526	US-10-094-749-1861	Sequence 1861, App
19	1415	61.2	431	US-10-000-039-2	Sequence 2, Appl
20	1415	61.2	431	US-10-353-690-12	Sequence 12, Appl
21	1415	61.2	431	US-10-756-149-5279	Sequence 5279, App
22	1415	61.2	431	US-11-044-570-2	Sequence 2, Appl
23	1411.5	61.1	430	US-09-810-808-9	Sequence 9, Appl
24	1411	61.1	431	US-09-810-808-5	Sequence 5, Appl
25	1392	60.2	594	US-10-732-923-10768	Sequence 10768, A
26	1390.5	60.2	433	US-10-732-923-10767	Sequence 10767, A
27	1342.5	58.1	340	US-10-217-574-17	Sequence 17, Appl

28	1342.5	58.1	340	4	US-10-217-555-17	Sequence 17, Appl
29	1328.5	57.5	429	4	US-10-295-027-116	Sequence 116, App
30	1328.5	57.5	496	3	US-09-764-875-746	Sequence 746, App
31	1328.5	57.5	496	3	US-09-764-875-900	Sequence 900, App
32	1328.5	57.5	496	5	US-10-737-450-4	Sequence 4, Appl
33	1326.5	57.4	496	3	US-09-784-249-2	Sequence 2, Appl
34	1317.5	57.0	496	4	US-10-755-889-42	Sequence 42, Appl
35	1164.5	50.4	308	4	US-10-664-421-85	Sequence 85, Appl
36	1164.5	50.4	308	5	US-10-941-635-85	Sequence 85, Appl
37	983	42.5	422	4	US-10-369-493-7027	Sequence 7027, App
38	891	38.6	479	3	US-09-771-161A-246	Sequence 246, App
39	891	38.6	479	3	US-09-771-161A-247	Sequence 247, App
40	891	38.6	479	3	US-09-771-161A-248	Sequence 248, App
41	891	38.6	479	4	US-10-394-322A-3	Sequence 3, Appl
42	891	38.6	479	4	US-10-217-574-33	Sequence 33, Appl
43	891	38.6	479	4	US-10-217-555-33	Sequence 33, Appl
44	891	38.6	479	5	US-10-753-267-108	Sequence 108, App
45	888.5	38.4	276	3	US-09-764-868-669	Sequence 669, App

ALIGNMENTS

RESULT 1

US-10-753-267-126
; Sequence 126, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriguez-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 36005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MPI03-003PIRNMNM
; CURRENT APPLICATION NUMBER: US/10753,267
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 427

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-753-267-126

Query Match      100.0%; Score 2311; DB 5; Length 427;
Best Local Similarity 100.0%; Pred. No. 1e-158;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQGLLTSGRKPSGGGRCCTGRGWRGQWCLKPMWGGADPPTPTLSCLLLPVPPPELPHCYR 60
Db 1 MQGLLTSGRKPSGGGRCCTGRGWRGQWCLKPMWGGADPPTPTLSCLLLPVPPPELPHCYR 60

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 120
Db 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 120

QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 180
Db 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 180

QY 181 LFFHLQRRERFLPRARFYAAEVAISAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240
Db 181 LFFHLQRRERFLPRARFYAAEVAISAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240

QY 241 CKEGVPEPDTTSTFCGTPEYLAPEVLKPEYDRAVDWMCCLGAVLYEMLHGLPPFYSDVVS 300
Db 241 CKEGVPEPDTTSTFCGTPEYLAPEVLKPEYDRAVDWMCCLGAVLYEMLHGLPPFYSDVVS 300

QY 301 QMYENILHQPLOIPGGRTVAACDLQSLHKKDQRLGSKADFLKKNHVFSPINWDDL 360
Db 301 QMYENILHQPLOIPGGRTVAACDLQSLHKKDQRLGSKADFLKKNHVFSPINWDDL 360

QY 361 YHKRLTPPNVNTGPDALKHFDPEFTQEAIVSKSIGCTPDTVASSGASSAFILGFSAYPE 420
Db 361 YHKRLTPPNVNTGPDALKHFDPEFTQEAIVSKSIGCTPDTVASSGASSAFILGFSAYPE 420

QY 421 DDILDC 427
Db 421 DDILDC 427

RESULT 2
US-10-262-511-140
; Sequence 140, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
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; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 140
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-140

Query Match      91.9%; Score 2124.5; DB 4; Length 398;
Best Local Similarity 93.2%; Pred. No. 2.8e-145;
Matches 398; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

QY 1 MQGLLTSGRKPSGGGRCCTGRGWRGQWCLKPMWGGADPPTPTLSCLLLPVPPPELPHCYR 60
Db 1 MQGLLTSGRKPSGGGRCCTGRGWRGQWCLKPMWGGADPPTPTLSCLLLPVPPPELPHCYR 60

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 120
Db 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNVGVLLAKRKSDDGAF 120

QY 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 180
Db 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDDYVNGGE 180

QY 181 LFFHLQRRERFLPRARFYAAEVAISAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240
Db 181 LFFHLQRRERFLPRARFYAAEVAISAIGYLHSLNIIYRDLKPNILLDCQGHVLTDFGL 240

QY 241 CKEGVPEPDTTSTFCGTPEYLAPEVLKPEYDRAVDWMCCLGAVLYEMLHGLPPFYSDVVS 300
Db 241 CKEGVPEPDTTSTFCGTPEYLAPEVLKPEYDRAVDWMCCLGAVLYEMLHGLPPFYSDVVS 300

QY 301 QMYENILHQPLOIPGGRTVAACDLQSLHKKDQRLGSKADFLKKNHVFSPINWDDL 360
Db 301 QMYENILHQPLOIPGGRTVAACDLQSLHKKDQRLGSKADFLKKNHVFSPINWDDL 360

QY 361 YHKRLTPPNVNTGPDALKHFDPEFTQEAIVSKSIGCTPDTVASSGASSAFILGFSAYPE 420
Db 361 YHKRLTPPNVNTGPDALKHFDPEFTQEAIVSKSIGCTPDTVASSGASSAFILGFSAYPE 420

QY 421 DDILDC 427
Db 421 DDILDC 398

RESULT 3
```

US-10-296-115-1109
; Sequence 1109, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hysaeq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1109
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1109
Query Match 86.8%; Score 2005; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.2e-136;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 53 ELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLA 112
Db 8 ELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLA 67
Qy 113 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFV 172
Db 68 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFV 127
Qy 173 LDYVNGGELFFHLQRRERFLEPRARFYAAEVAASAGYLHSLNIYRDLKPENILLDCQGH 232
Db 128 LDYVNGGELFFHLQRRERFLEPRARFYAAEVAASAGYLHSLNIYRDLKPENILLDCQGH 187
Qy 233 VLTDFGLCKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLP 292
Db 188 VLTDFGLCKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLP 247
Qy 293 PFYSQDVSMYENILHQPLOIPGRTVAACDLILQSLHKKDQORLGSKADFLKIKNHVFF 352
Db 248 PFYSQDVSMYENILHQPLOIPGRTVAACDLILQSLHKKDQORLGSKADFLKIKNHVFF 307
Qy 353 SPINWDDLHKRLTTPFPNPNVTGPADLKHFPDPEFTQEAUSKSICTPDTVASSSGASSAF 412
Db 308 SPINWDDLHKRLTTPFPNPNVTGPADLKHFPDPEFTQEAUSKSICTPDTVASSSGASSAF 367
Qy 413 LGFSYAPEDDDIILDC 427
Db 368 LGFSYAPEDDDIILDC 382
RESULT 4
US-10-296-543-83
; Sequence 83, Application US/10926543
; Publication No. US20050048589A1
; GENERAL INFORMATION:
; APPLICANT: Jendoubi, Moncef
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCE, THEIR
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND DISEASE
; TITLE OF INVENTION: MANAGEMENT OF LUNG CANCER
; FILE REFERENCE: 705403.4004
; CURRENT APPLICATION NUMBER: US/10/926,543
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US 60/497,790
; PRIOR FILING DATE: 2003-08-25
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-926-543-83
Query Match 86.8%; Score 2005; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.2e-136;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 53 ELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLA 112
Db 22 ELPDHCYRMNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLA 81
Qy 113 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFV 172
Db 82 KRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFV 141
Qy 173 LDYVNGGELFFHLQRRERFLEPRARFYAAEVAASAGYLHSLNIYRDLKPENILLDCQGH 232
Db 142 LDYVNGGELFFHLQRRERFLEPRARFYAAEVAASAGYLHSLNIYRDLKPENILLDCQGH 201
Qy 233 VLTDFGLCKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLP 292
Db 202 VLTDFGLCKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLP 261
Qy 293 PFYSQDVSMYENILHQPLOIPGRTVAACDLILQSLHKKDQORLGSKADFLKIKNHVFF 352
Db 262 PFYSQDVSMYENILHQPLOIPGRTVAACDLILQSLHKKDQORLGSKADFLKIKNHVFF 321
Qy 353 SPINWDDLHKRLTTPFPNPNVTGPADLKHFPDPEFTQEAUSKSICTPDTVASSSGASSAF 412
Db 322 SPINWDDLHKRLTTPFPNPNVTGPADLKHFPDPEFTQEAUSKSICTPDTVASSSGASSAF 381
Qy 413 LGFSYAPEDDDIILDC 427
Db 382 LGFSYAPEDDDIILDC 396
RESULT 5
US-09-971-118-2
; Sequence 2, Application US/09971118
; Patent No. US20020123056A1
; GENERAL INFORMATION:
; APPLICANT: DELANEY, ALLEN
; APPLICANT: YOGANATHAN, THILLAINATHAN
; TITLE OF INVENTION: SGK2 AND ITS USES
; FILE REFERENCE: KINE025CIP
; CURRENT APPLICATION NUMBER: US/09/971,118
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/21479
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-118-2
Query Match 84.6%; Score 1954; DB 3; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.3e-133;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRSDGAF 120
Db 1 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNKGVLLAKRSDGAF 60
Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYNGGE 180
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPPFLVGLRYSFQTPKLYFVLDYNGGE 120
Qy 181 LFFHLQRRERFLEPRARFYAAEVAASAGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 240
Db 121 LFFHLQRRERFLEPRARFYAAEVAASAGYLHSLNIYRDLKPENILLDCQGHVLTDFGL 180

QY 241 CKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVVS 300
DB 181 CKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVVS 240
QY 301 QMYENILHQPLOIPGGRITVAACDLQLSLHKKDQORLGSKADPLEIKNVHVFSPINWDDL 360
DB 241 QMYENILHQPLOIPGGRITVAACDLQLSLHKKDQORLGSKADPLEIKNVHVFSPINWDDL 300
QY 361 YHKRLTPPNPNVTGPADLKHDFEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 420
DB 301 YHKRLTPPNPNVTGPADLKHDFEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 421 DDDILDC 427
DB 361 DDDILDC 367

RESULT 6
US-10-291-172-256
; Sequence 256, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 256
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-256

Query Match 84.6%; Score 1954; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.3e-133; Mismatches 0; Indels 0; Gaps 0;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 120
DB 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60
QY 121 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGE 180
DB 61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGE 120
QY 181 LFFHLQRRERFLPRARFYAAEVAASAIQYLHLSNIIYRDLKPENILLDCQGHVLLTDFGL 240
DB 121 LFFHLQRRERFLPRARFYAAEVAASAIQYLHLSNIIYRDLKPENILLDCQGHVLLTDFGL 180
QY 241 CKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVVS 300
DB 181 CKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVVS 240
QY 301 QMYENILHQPLOIPGGRITVAACDLQLSLHKKDQORLGSKADPLEIKNVHVFSPINWDDL 360
DB 241 QMYENILHQPLOIPGGRITVAACDLQLSLHKKDQORLGSKADPLEIKNVHVFSPINWDDL 300
QY 361 YHKRLTPPNPNVTGPADLKHDFEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 420
DB 301 YHKRLTPPNPNVTGPADLKHDFEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 360

DB 301 YHKRLTPPNPNVTGPADLKHDFEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 421 DDDILDC 427
DB 361 DDDILDC 367
RESULT 7
US-10-429-160-52
; Sequence 52, Application US/10429160
; Publication No. US20040023276A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Teresa R
; APPLICANT: Mao, Mao
; APPLICANT: Linsley, Peter S
; APPLICANT: Lund, Lund
; TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
; FILE REFERENCE: RS0200
; CURRENT APPLICATION NUMBER: US/10/429,160
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/377,714
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-160-52

Query Match 84.6%; Score 1954; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.3e-133; Mismatches 0; Indels 0; Gaps 0;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 120
DB 1 MNSSPAGTSPQPSRANGINILGPSANPNAQPTDFDLKVIKGNKGVLLAKRKS DGAF 60
QY 121 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGE 180
DB 61 YAVKVLQKKSILKKKQSHIMAERSVLLKNVRHPLVGLRYSQTPEKLYFVLDDYNGGE 120
QY 181 LFFHLQRRERFLPRARFYAAEVAASAIQYLHLSNIIYRDLKPENILLDCQGHVLLTDFGL 240
DB 121 LFFHLQRRERFLPRARFYAAEVAASAIQYLHLSNIIYRDLKPENILLDCQGHVLLTDFGL 180
QY 241 CKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVVS 300
DB 181 CKEGVEPEDTTSTFCGTPYLAPEVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVVS 240
QY 301 QMYENILHQPLOIPGGRITVAACDLQLSLHKKDQORLGSKADPLEIKNVHVFSPINWDDL 360
DB 241 QMYENILHQPLOIPGGRITVAACDLQLSLHKKDQORLGSKADPLEIKNVHVFSPINWDDL 300
QY 361 YHKRLTPPNPNVTGPADLKHDFEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 420
DB 301 YHKRLTPPNPNVTGPADLKHDFEFTQEAHSVKSIGCTPDTVASSSGASSAFLGFSYAPE 360
QY 421 DDDILDC 427
DB 361 DDDILDC 367

RESULT 8
US-10-221-278-256
; Sequence 256, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 256
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-256

Query Match 84.6%; Score 1954; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.3e-133;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	61	MNSSPAGTSPQPSRANGNINLGP	SNPNAQPTDFDLKVGKNGYKVLLAKR	SDGAF	120
Db	1	MNSSPAGTSPQPSRANGNINLGP	SNPNAQPTDFDLKVGKNGYKVLLAKR	SDGAF	60
Qy	121	YAVKVLQKKSILKKKQSHIMAERSV	LLKNVRHPFLVGLRYSFQTPKLYFVLDY	VNGGE	180
Db	61	YAVKVLQKKSILKKKQSHIMAERSV	LLKNVRHPFLVGLRYSFQTPKLYFVLDY	VNGGE	120
Qy	181	LFPHLQRRERFLPRARFYAAEVA	SAIGYLHSLNIIYRDLKPNILLDCQGHV	VLDTFGL	240
Db	121	LFPHLQRRERFLPRARFYAAEVA	SAIGYLHSLNIIYRDLKPNILLDCQGHV	VLDTFGL	180
Qy	241	CKEGVEPEDTSTFCGTPYLAPEV	LKPEPYDRAVDWMCGLGAVLYEMLHGL	PPFYSQDVS	300
Db	181	CKEGVEPEDTSTFCGTPYLAPEV	LKPEPYDRAVDWMCGLGAVLYEMLHGL	PPFYSQDVS	240
Qy	301	QMYENILHQPLOIPGGRTVAACD	LLOSLHLKQORLGSKADFLKKNHVF	FSPIINWDDL	360
Db	241	QMYENILHQPLOIPGGRTVAACD	LLOSLHLKQORLGSKADFLKKNHVF	FSPIINWDDL	300
Qy	361	YHKRLTPFPNPVNTGADLKHFDP	EFTQEA VSKSIGCTPTDVASSG	SAFLGFSVAPE	420
Db	301	YHKRLTPFPNPVNTGADLKHFDP	EFTQEA VSKSIGCTPTDVASSG	SAFLGFSVAPE	360
Qy	421	DDDLDC	427		
Db	361	DDDLDC	367		

RESULT 9
US-10-380-235-6
; Sequence 6, Application US/10380235
; Publication No. US20040072184A1
; GENERAL INFORMATION:
; APPLICANT: Yoganathan, Thillainathan
; APPLICANT: Delaney, Allen
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND
; TITLE OF INVENTION: THEIR USES
; FILE REFERENCE: KINE-024CIP
; CURRENT APPLICATION NUMBER: US/10/380,235
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: IB01/02237
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/290,555
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/233,999
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,423

; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/238,558
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-235-6

Query Match 84.6%; Score 1954; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.3e-133;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	61	MNSSPAGTSPQPSRANGNINLGP	SNPNAQPTDFDLKVGKNGYKVLLAKR	SDGAF	120
Db	1	MNSSPAGTSPQPSRANGNINLGP	SNPNAQPTDFDLKVGKNGYKVLLAKR	SDGAF	60
Qy	121	YAVKVLQKKSILKKKQSHIMAERSV	LLKNVRHPFLVGLRYSFQTPKLYFVLDY	VNGGE	180
Db	61	YAVKVLQKKSILKKKQSHIMAERSV	LLKNVRHPFLVGLRYSFQTPKLYFVLDY	VNGGE	120
Qy	181	LFPHLQRRERFLPRARFYAAEVA	SAIGYLHSLNIIYRDLKPNILLDCQGHV	VLDTFGL	240
Db	121	LFPHLQRRERFLPRARFYAAEVA	SAIGYLHSLNIIYRDLKPNILLDCQGHV	VLDTFGL	180
Qy	241	CKEGVEPEDTSTFCGTPYLAPEV	LKPEPYDRAVDWMCGLGAVLYEMLHGL	PPFYSQDVS	300
Db	181	CKEGVEPEDTSTFCGTPYLAPEV	LKPEPYDRAVDWMCGLGAVLYEMLHGL	PPFYSQDVS	240
Qy	301	QMYENILHQPLOIPGGRTVAACD	LLOSLHLKQORLGSKADFLKKNHVF	FSPIINWDDL	360
Db	241	QMYENILHQPLOIPGGRTVAACD	LLOSLHLKQORLGSKADFLKKNHVF	FSPIINWDDL	300
Qy	361	YHKRLTPFPNPVNTGADLKHFDP	EFTQEA VSKSIGCTPTDVASSG	SAFLGFSVAPE	420
Db	301	YHKRLTPFPNPVNTGADLKHFDP	EFTQEA VSKSIGCTPTDVASSG	SAFLGFSVAPE	360
Qy	421	DDDLDC	427		
Db	361	DDDLDC	367		

RESULT 10
US-10-131-410-104
; Sequence 104, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-104

Query Match 61.5%; Score 1421.5; DB 4; Length 388;


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; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD01
US-09-981-353-7

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Query Match	61.4%;	Score 1419;	DB 3;	Length 431;
Best Local Similarity	68.3%;	Pred. No. 3e-94;		
Matches 267;	Conservative 56;	Mismatches 54;	Indels 14;	Gaps 4;
Qy	38	PPTPTLSCLLLPVPELPDHCYRMNSSPAGTSPSPQSRANGINILGPSANNAOPTD	DF	97
Db	52	PEVOSILKISQPPEL-----NNANP--SPPSPSQ---QINLGPSNHPAKSPD	PHF	100
Qy	98	LKVIKGNGYKVLAKRSKGAFYAVKVLQKKSILKKKEQSHIMAEKRSVLKKNVRHP	PLV	157
Db	101	LKVIKGSGFGKVLARHKAEEVFYAVKVLQKKAILLKKKEKHIMSEKRVLLKNVKHP	PLV	160
Qy	158	GLRYSFOTPEKLYFVLDYVNGGELFFHLORRRFLEPRARYAAEVAASAIQYLS	LNII	217
Db	161	GLHFSQTADKLYFVLDYINGELFYHLQRCFLEPRARYAAEIASALGYLS	LNIV	220
Qy	218	RLDKPENILLDCQGHVLTDFGLCKEGVEPDDTSTFCGTEPYLAPEVLRKEP	VDRAVDM	277
Db	221	RLDKPENILLDSQGHVLTDFGLCKENIEHNSTTSTFCGTEPYLAPEVLRKHQ	PDRTVDM	280
Qy	278	WCLGAVLYEMLHGULPPFYQDVQSWYENILHQPIQIPGGRTVAAACDLQSL	LLHKDQQRRL	337
Db	281	WCLGAVLYEMLYGLPPFYSRNTAEYMDNILNKLPLQKLPNTNSARHLL	EGLLQDRKRL	340
Qy	338	GSKADFLIEIKNHVFSPINDDLVHKRLTPFPFNPNVTGPADLKHFDDEFT	CEAVSKSG	397
Db	341	GAKDDFWEIKSHVFSLINDDLLINKKITPFPFNVPNSGPNDLRHFDEFT	EEEPVNSIGK	400
Qy	398	TPDPTV---ASSSGASSAFLGFSYAPEDDDIL		425
Db	401	SPDSVLVTASVKEAAEAFLGFSYAPDTSFL		431

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RESULT 14
US-10-403-161-2
; Sequence 2, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08

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; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 2
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-2

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Query Match	61.4%;	Score 1419;	DB 4;	Length 431;
Best Local Similarity	68.3%;	Pred. No. 3e-94;		
Matches 267;	Conservative 56;	Mismatches 54;	Indels 14;	Gaps 4
Qy	38	PPTPTSLCLLPVPELPDHCYRMNSSPAGTPSPQPRANGININLGPSANNAOPTD	97	
Db	52	PEVQSILKISQPEPEL-----NNANP--SPPPSPSQ--QINLGSSNPHAKSPDHF	100	
Qy	98	LKVTKGNYGKVLAKKSGDAFYAVKVLQKKSILKKKEQSHIMAEBSVLAKNVHPFLV	157	
Db	101	LKVTKGSGFGKVLARHAKBEVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLV	160	
Qy	158	GLRYSFOTPEKLYFLVDYVNGELFFHLQREERTLEPRARYAEVASAIGVLSHLNIIV	217	
Db	161	GLHFSFQADKLYFLVDYINGELFFHLQRECRCTLEPRARYAEIASGALGVLSHLNIIV	220	
Qy	218	RLDKPENILLDCQGHVLTDFGLCKEGVEPEDTSTTCGTPHYLAPEVLRKEPYDRAVDM	277	
Db	221	RLDKPENILLDSQGHIVLTDGLCKENIEHNSTTSTTCGTPHYLAPEVLHQPYDRTVDM	280	
Qy	278	WCLGAVLYEMLHGLPPYSDQSVOMYENILHQPIQIPGGRTVAACDLLQSLHDKQORQL	337	
Db	281	WCLGAVLYEMLYGLPPYFSYRNTAEYMINLKPLQLKPNITNSARHLLGLEGLQDKRTKL	340	
Qy	338	GSKADFLIEIKNHVFFSPINWDDLHKLLTPFPNPNVTGPADLKHFDPEFTCEAVSKSGC	397	
Db	341	GAKDDFWEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLRHFDPEFTPEEPVNSICK	400	
Qy	398	TPDPTV---ASSSGASSAFLGFSYAPEDDDIL	425	
Db	401	SPDSVLVTASVKAEAAEALFGFSYAPPTDSFL	431	

RESULT 15
US-10-403-161--4
Sequence 4, Application US/10403161
Publication No. US20040043930A1
GENERAL INFORMATION:
APPLICANT: Anderson, David et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-573C
CURRENT APPLICATION NUMBER: US/10/403,161
CURRENT FILING DATE: 2003-03-31
PRIORITY APPLICATION NUMBER: 60/370349
PRIORITY FILING DATE: 2002-04-05
PRIORITY APPLICATION NUMBER: 60/384543
PRIORITY FILING DATE: 2002-05-30
PRIORITY APPLICATION NUMBER: 60/370969
PRIORITY FILING DATE: 2002-04-08
PRIORITY APPLICATION NUMBER: 60/403748
PRIORITY FILING DATE: 2002-08-15
PRIORITY APPLICATION NUMBER: 60/372019
PRIORITY FILING DATE: 2002-04-12
PRIORITY APPLICATION NUMBER: 60/374379
PRIORITY FILING DATE: 2002-04-22
PRIORITY APPLICATION NUMBER: 09/779679
PRIORITY FILING DATE: 2001-02-08
PRIORITY APPLICATION NUMBER: 60/181045
PRIORITY FILING DATE: 2000-02-08
PRIORITY APPLICATION NUMBER: 10/055877

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; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-4

Query Match      61.4%; Score 1419; DB 4; Length 431;
Best Local Similarity 68.3%; Pred. No. 3e-94;
Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 38 PPTPTLSCLLPVPPELPHCYRMNSPAGTSPQPSRANGNINLGPSANPNAPTDFDF 97
Db 52 PEVQSILKISQPEPEL-----MNANP--SPPPSQ---QINLGSSNPHAKPSDFHF 100

QY 98 LKVIKGNVGVKLLAKRKSDGAFYAVKVLQKKSILKKKQSHIMABERSVLLKNVRHPFLV 157
Db 101 LKVIKGSFGKVLARHKAEEVYAVKVLQKKAILEKKEKIMSERNVLLKNVKHPFLV 160

QY 158 GLRYSQTPEKLYFVLVDYNGGELFHLQREERFLEPRARFYAAEVAISALGYLHSLNIY 217
Db 161 GLHFSQTADKLYFVLVDYNGGELFHLQREERFLEPRARFYAAEVAISALGYLHSLNIY 220

QY 218 RDLKPENILLDCGHVVLTDGFCCKEGVEPEDTSTFCGTPEYLAPEVLRKEPYDRAVDW 277
Db 221 RDLKPENILLDSQGHIVLTDGFCCKENIEHNSTSTFCGTPEYLAPEVLRKEPYDRTVDW 280

QY 278 WCLGAVLYEMLHGLPPFYSDQVSQMYENILHQPLOIPGGRTVAACDLQSLHKKQORQL 337
Db 281 WCLGAVLYEMLYGLPPFYSRNTAEMYDNLINKPLQLKPNITNSARHLEGLLQKDRKRL 340

QY 338 GSKADPLEIKNHVFFSPINWDDLHKRLTTPPNPNVTGPADLKHDFDPEETOEAIVSKSICG 397
Db 341 GAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPNDLRHFDPEETEEPPVNSIGK 400

QY 398 TPDVTV---ASSSGASSAFLGFSYAPEDDDIL 425
Db 401 SPDVLVTASVKEAEAFLGFSYAPTDSFL 431
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Search completed: January 27, 2006, 23:57:33
Job time : 74.9264 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:32:16 ; Search time 11.0107 Seconds
(without alignments)
419.957 Million cell updates/sec

Title: US-09-868-131A-8

Perfect score: 2311

Sequence: 1 MQGLTSGRKPSGGGRCTGR.....ASSAFLGFSYAPEDDDILDC 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1419	61.4	543	6	US-10-821-234-1158
2	874.5	37.8	480	7	US-11-109-156-18
3	788.5	34.1	495	6	US-10-770-726-81
4	765	33.1	737	7	US-11-152-366-28
5	722.5	31.3	740	6	US-10-878-556A-129
6	713.5	30.9	942	6	US-10-770-726-76
7	705.5	30.5	341	7	US-11-092-168-4
8	694.5	30.1	343	7	US-11-092-168-3
9	694.5	30.1	351	7	US-11-132-142-13
10	694.5	30.1	462	7	US-11-132-142-10
11	691.5	29.9	351	7	US-11-132-142-14
12	681.5	29.5	350	6	US-10-497-767-4
13	681.5	29.5	381	7	US-11-132-142-9
14	681	29.5	705	6	US-10-995-561-856
15	681	29.5	706	6	US-10-995-561-855
16	681	29.5	706	7	US-11-099-958-1
17	679	29.4	331	7	US-11-099-958-2
18	675	29.2	353	7	US-11-132-142-11
19	672.5	29.1	395	7	US-11-132-142-12
20	670	29.0	515	7	US-11-132-142-8
21	662	28.6	398	7	US-11-132-142-7
22	649.5	28.1	548	7	US-11-132-142-5
23	644	27.9	480	7	US-11-132-142-6
24	547	23.7	637	7	US-11-113-837-4
25	541.5	23.4	1732	6	US-10-055-877-147

26	536	23.2	756	7	US-11-113-837-20	Sequence 20, Appl
27	535.5	23.2	1663	6	US-10-055-877-148	Sequence 148, App
28	532.5	23.0	1590	6	US-10-055-877-146	Sequence 146, App
29	529	22.9	635	7	US-11-113-837-16	Sequence 16, Appl
30	528	22.8	256	6	US-10-877-346-72	Sequence 72, Appl
31	528	22.8	256	7	US-11-113-424-183	Sequence 183, App
32	527.5	22.8	1197	6	US-10-055-877-8	Sequence 8, Appl
33	527.5	22.8	1247	6	US-10-055-877-10	Sequence 10, Appl
34	508	22.0	688	7	US-11-113-424-45	Sequence 45, Appl
35	506	21.9	1613	6	US-10-055-877-145	Sequence 145, App
36	506	21.9	1637	6	US-10-055-877-144	Sequence 144, App
37	502.5	21.7	668	7	US-11-113-424-12	Sequence 12, Appl
38	502	21.7	598	7	US-11-113-837-18	Sequence 18, Appl
39	502	21.7	639	7	US-11-113-837-21	Sequence 21, Appl
40	499	21.6	688	7	US-11-113-424-48	Sequence 48, Appl
41	498.5	21.6	665	7	US-11-113-837-19	Sequence 19, Appl
42	491	21.2	688	7	US-11-113-424-49	Sequence 49, Appl
43	489	21.2	396	7	US-11-125-295-11	Sequence 11, Appl
44	489	21.2	407	7	US-11-125-295-9	Sequence 9, Appl
45	483	20.9	689	7	US-11-113-424-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-821-234-1158
; Sequence 1158, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1158
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1158

Query Match	61.4%	Score 1419;	DB 6;	Length 543;
Best Local Similarity	68.3%	Pred. No. 1.7e-112;		
Matches	267;	Conservative	56;	Mismatches 54;
				Indels 14;
				Gaps 4;
QY	38	PPTPTUSCLLLPVPELPDHCYMNSSPAGTPSPQSRANGNINLGPANPNQPTDFD	97	
Db	164	PEVQSILKISQPOPEL-----MNANP--SPPPSPSQ---QINLGPSSPHAKPSDFH	212	
QY	98	LKVIKGNVGVLLAKKSDGAFYAVKVLQKKSILKKQSHIMASRSVLLKNVHPFLV	157	
Db	213	LKVIKGSFGKVLARHAEVYAVKVLQKKAIIKKKEKIMSRNVLKNVHPFLV	272	
QY	158	GLRYSFQTPEKLYFVLDYVNGGELFPHLQRRERFLPRFARFYAAEASAIYLHSLNIIY	217	
Db	273	GLHFSQTADKLYFVLDYINGGELFYHLQRCFLPRFARFYAAEASAIYLHSLNIVY	332	
QY	218	RLDKPENILLDCGHVLLTDFGLCKEGVEPEDTSTFCGTPPEYLAPEVLKPYDRAVDW	277	
Db	333	RLDKPENILLDSQGHVLLTDFGLCKENIEHNSTTSTFCGTPPEYLAPEVLKPYDRTVDW	392	
QY	278	WCLGAVLYEMHCLPPFYSDVSOYENILHOPLOIPGGRTVAACDLQSLHKKDQRL	337	
Db	393	WCLGAVLYEMHCLPPFYSDVSOYENILHOPLOIPGGRTVAACDLQSLHKKDQRL	452	
QY	338	GSKADFLKINHVFFSPINWDDLYHKRLTTPPNPNVTGPADLKHDFPEFTQEAHSVKSIGC	397	

Db 453 GAKDDFMEIKSHVFFSLINWDDLLNKITPPFPNPNVSGNDLRHDFDPEFTPEEPVPSIGK 512
QY 398 TPDVT---ASSSGASSAFLGFSYAPEDDDIL 425
Db 513 SPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 543
RESULT 2
US-11-109-156-18
; Sequence 18, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/Jp00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-18
Query Match 37.8%; Score 874.5; DB 7; Length 480;
Best Local Similarity 47.5%; Pred. No. 1.5e-66;
Matches 174; Conservative 59; Mismatches 102; Indels 31; Gaps 7;
QY 66 AGTPSPQSPRANGINILGPSANPNAQPT--DPDFLKVIGKNGYKVLAKRKSDDGAFYAV 123
Db 122 SGSPSDNSGAEVSL--AKPKHRTVNEFEYLLKLGKGTGKVLVKEKATGRYAM 178
QY 124 KVLQKSLIKKKQSHIMAEVSLLKNVRHPFLVGLRYSGFQTPKLYFVLVDYVNGGELFF 183
Db 179 KILKKEVIVAKDEVATLTENRV-LQNSRHPFTALKYSFQTHDRLCFVMEYANGELFP 237
QY 184 HLQRRERFLEPRARFYAAEVASAIYGLHS-LNTIYRDLKPENILLDCQGHVLTDFGLCK 242
Db 238 HLSRERVFSDRARFYGAETVSALDYHSEKNVVYRDLKLENMLDKDGHIKITDFGLCK 297
QY 243 EGVPEPDTTSTFCGTEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVSQM 302

Db 298 EGKOGATMKTTCGTEYLAPVLENDYGRAVDWMLGLGVMTYEMMCGRLPFFYNQDHEKL 357
QY 303 YENILHQPLQIPGGRVTAACDLLQSLHLHQDQRL-GSKADFLIEIKNHVFFSFSPINDDLY 361
Db 358 FELLIMEEIRFRTLGPPEAKSLLSGLLKKDKPQRLGGSSDAKEIQHRRFFAGIVQHVVY 417
QY 362 HKRLTPPNPNTVGPADLKHDFPEFTQEAUVSSKSGICTPDTVASSSGASSAFLGFSYAPED 421
Db 418 EKKLSPPFPQVTSSETDTRYDEEFTAQMIT-----ITP-----PDQ 454
QY 422 DDILDC 427
Db 455 DDSMEC 460
RESULT 3
US-10-770-726-81
; Sequence 81, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-81
Query Match 34.1%; Score 788.5; DB 6; Length 495;
Best Local Similarity 45.8%; Pred. No. 3e-59;
Matches 162; Conservative 64; Mismatches 111; Indels 17; Gaps 8;
QY 79 NINLGPSANPNAQPTDFDLKLVIGKNGYKVLAKRKSDD--GAFYAVKVLQKKSILKK- 134
Db 67 SVNVGPE---RIGPHCFELLRVIGKGYKVFQVRKVGQTNLGIYAMKVLRAKIVRNA 123
QY 135 KEQSHIMAEVSLLKNVRHPFLVGLRYSGFQTPKLYFVLVDYVNGGELFFHLQRRERFLEP 194
Db 124 KDTAHTRAERNI-LESVKHPFIVELAYAFQTGKLYLLECLSGGELFTHLREGIFLED 182
QY 195 RARFYAAEVASAIYGLHSLNIIYRDLKPENILLDCQGHVLTDFGLCKGVEPEDTTSIF 254
Db 183 TACFYLAETITLALGHLHSQGIYRDLKPENIMLSQSGHIKLTDFGLCKESIHEGAVTHTF 242
QY 255 CGTPEYLAPVLRKEPYDRAVDWMLGAVLYEMLHGLPPFYSDVSQMVENILHQPLQIP 314
Db 243 CGTIEYMAPEILVRSGHNRAVDWMLGALMYDMLTGSPPPTAENRRKTKDKIIRGKLALP 302
QY 315 GGRVTAACDLLQSLHLHQDQRL-GSKADFLIEIKNHVFFSFSPINDDLYHKRLTTPPNPV 373
Db 303 PYLTPDARDLVKKFLKRNPSQRIKGGPGDAADVQRHPFFRHMWDDLLAWRDPFPRPCL 362
QY 374 TGPADLKHDFPEFTQEAUVSSKSGICTPDTVASSSGASSAFLGFSY-APEDDDIIL 426
Db 363 QSEEDVSQPTDTRFTQTPTPVS----PDDTALSANQAFGLGTYVAP---SVLD 409
RESULT 4
US-11-152-366-28
; Sequence 28, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
; APPLICANT: Bvgs, Reginald
; APPLICANT: Vandeghinste, Nick

APPLICANT: Tomme, Peter H. M.
TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
TREATMENT OF Degenerative & Inflammatory Diseases
FILE REFERENCE: P27,980-A USA
CURRENT APPLICATION NUMBER: US/11/152,366
CURRENT FILING DATE: 2005-06-14
PRIORITY FILING DATE: 60/579,307
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 295
SOFTWARE: Patent in version 3.3
SEQ ID NO 28
LENGTH: 737
TYPE: PRT
ORGANISM: Homo sapiens
US-11-152-366-28

Query Match 33.1%; Score 765; DB 7; Length 737;
Best Local Similarity 42.3%; Pred. No. 4.8e-57;
Matches 159; Conservative 67; Mismatches 120; Indels 30; Gaps 6;

QY 59 YRNSSPAG-TPSPQPSRANGNINLGPANPNAQPTDFDLKVGKGYKVLAKKSD 117
Db 376 HRAASSPDGQMLSP---GENGEVRQQAQKRLGLD--EFNFIKVLKGSFGKVMIAELKKG 430
QY 118 GAFYAVKVLQKKSILKKEQSHIMAERSVLLKNVRHFLVGLRYSFQTPEKLYFVLDYVN 177
Db 431 DEVYAVKVLKQDVLQDDVDCTMTKRIILALARKHLYLTQLYCCFQTKDRLFFVMEYVN 490
QY 178 GGELFPHLQERFLERARFYAAEASATGYLHSLNIIYRDLKPNILLDCQGHVLTLD 237
Db 491 GGDLMFQIQRKFRDESRFYAAEAVTSALMFLHQHVIYRDLKDNILLDAEGHCKLAD 550
QY 238 FGLCKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGLPPYSQ 297
Db 551 FGCKEGLNGVTTTFCGTPDIAPILQELGYGSDVWALGVLMYEMAQPPPEAD 610
QY 298 DVSQMVENILHQLQIPGGRTVAACDLQSLHLKQKRLG---SKADFLFIKKNHVFVFP 354
Db 611 NEDDLFESILHDDVLPVWLSKEAVSILKAFMTKNPKHRLGCVASQNGEDAIKQHPFFE 670
QY 355 INWDDLKHLTTPFPNPNVTGPADLKHFDPEFTQ-----EAVSKSIGCTPTDVTASS 405
Db 671 IDWVLEQKKIKPFKPRIKTRDVANFDQDFTREBPVLTLDVDEAIVKQIN----- 721
QY 406 SGAASSAFLGFSYAPED 421
Db 722 ---QEEFKGFSYGED 734

RESULT 5
US-10-878-556A-129
Sequence 129, Application US/10878556A
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patent in version 3.1
SEQ ID NO 129
LENGTH: 740
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw hum/k6a3_human
DATABASE ENTRY DATE: 1996-10-01
US-10-878-556A-129

Query Match 31.3%; Score 722.5; DB 6; Length 740;
Best Local Similarity 44.4%; Pred. No. 1.9e-53;
Matches 151; Conservative 58; Mismatches 118; Indels 13; Gaps 6;

QY 90 AQPTEDFDLKVGKGYKVLAKKSDG---AFYAVKVLQKKSILKKEQSHIMAERSV 146
Db 63 ADSQFELLKVLGQSGFGKVLVKISGSARQIYANKVL-KKATLKVDRVTRTMRDI 121
QY 147 LLKNVRHFLVGLRYSFQTPEKLYFVLDYVNGSELFFHLQRRRFLPRARFYAAEVASA 206
Db 122 LVE-VNHPFTVKLHYAFQTEGKLYLILDFLRGDGLFRLSKVMFTEDVKFYLAELALA 180
QY 207 IGYLHSLNIIYRDLKPNILLDCQGHVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPVL 266
Db 181 LDHLHSLGIIYRDLKPNILLDEGHILKLTDFGLSKESIDHEKKAVSFCGTVEYMAPEV 240
QY 267 RKEPYDRAVDWCLGAVLYEMLHGLPPYSQVSMYENILHQPLOIQCGRITVAACDLQ 326
Db 241 NREGHTQSADWNSFGVLMFEMLTGTLPFGQKDRKETMTMLKAKLGNPQLSPEAQSLLR 300
QY 327 SLHLKQORQLGSKADFL-EIKNVHVFSPINWDDLYHKRLTPFPNPNVTGPADLKHFDPE 385
Db 301 MLFKNPANRLGAGPDGVEIKRHSFSTIDMNKLYRREIHPFPKATGRPDTFYDPDE 360
QY 386 FTQEAIVSKSIGCTPTDVTASSSGASSAFLGFSYA--PEDDD 423
Db 361 FTAKTPKDSGPIPP-----SANAHQLFRGFSFAITSDDE 395

RESULT 6
US-10-770-726-76
Sequence 76, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patent in version 3.2
SEQ ID NO 76
LENGTH: 942
TYPE: PRT
ORGANISM: Homo sapiens
US-10-770-726-76

Query Match 30.9%; Score 713.5; DB 6; Length 942;
Best Local Similarity 38.5%; Pred. No. 1.5e-52;
Matches 165; Conservative 69; Mismatches 160; Indels 35; Gaps 10;

QY 3 GLLTSGRKPSGGGRCCTG-----RGGWRGQWCLKPMWGGADPPPTLSCLLLPV-----PPE 53
Db 530 GTFSPGASPGSEARTTGDISVEKLNLTGDSDSPQKSSRDPPS-SPSSLSPIQESTAPE 588
QY 54 LPDHCYRMNSSPAGTSPQPSRANGNINLGPANPNAQPTDFDLKVGKGYKVLAK 113
Db 589 LP-----SETQTEGP-----ALCSPLKSPILTLEDKFLAVLGRHGFVKVLLSE 633
QY 114 RKSDGAFYAVKVLQKKSILKKEQSHIMAERSV--LKNVRHFLVGLRYSFQTPEKLYF 171
Db 634 FRPSGELFAIKALKKGDIVARDEVESLMCEKRIILAAVTSAGHPFLVNLFCFQTPPEHVC 693
QY 172 VLDYVNGGELFFHLQRRRFLERARFYAAEASATGYLHSLNIIYRDLKPNILLDCQ 231
Db 694 VMEYSAGDMLHLHSD-VFSEPRATFYACVVLGQFLHEHKIVYRDLKDLNLLDTEG 752
QY 232 HVVLTDFGLCKEGVEPEDTTSTFCGTPPEYLAPVLRKEPYDRAVDWCLGAVLYEMLHGL 291
Db 753 YKVIADFLCKGMGVDRTSTFCGTPPEFLAPEVLTDTSYTRAVDWGLGVLYEMLVGE 812
QY 292 PPFYSDVSMYENILHQPLOIQCGRITVAACDLQSLHLKQKRLG-SKADFLFIKKNH 350

Db 813 SPFFGDDEEVDSIYNDEVRYPRFLSAEAGIMWRLLRRNPERRLLSSSERRDAEDVKQP 872
QY 351 FFSPIWDDLYHKRLTPFPNVTGPADLKHDPDEFTQEA--VSKSIGCTPDPVTVASSGA 408
Db 873 FFRTLGWEALLARRLPPFPVPTLSGRDVSNFDEEFTGEAPTILSPPRDARPLTAAB----- 928
QY 409 SSAFLGFSY 417
Db 929 QAAFLDPDF 937

RESULT 7
US-11-092-168-4
; Sequence 4, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bearss, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-092-168-4

Query Match 30.5%; Score 705.5; DB 7; Length 341;
Best Local Similarity 44.1%; Pred. No. 1.9e-52;
Matches 138; Conservative 63; Mismatches 105; Indels 7; Gaps 5;
QY 84 PSANPNAQPTDFDLKVIKGNVGVKLLAKRKS DGAFYAVKVLQKKSILKKKEQSHIMAE 143
Db 24 PSQN-TAQLDQPERIKTLGTSGFGRVNLVKHKS GNHYAMKILDKQKVKLKQIEHTLNE 82
QY 144 RSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGELFFHLQRRRFLPRARFYAAEV 203
Db 83 KRI-LQAVNFPFLVKLEFSFKDNLNMYMVEYVAGGEMFSLRRIGRFAEPHARFYAAQI 141
QY 204 ASAIGVLSLNIYRDLKPNILLDCQGHVLLTDGCLCKEGVEPDETTSTFCGTPPYLAP 263
Db 142 VLTFEYLSLDLIYRDLKPNILLDQGGYIQVTDFGFAK---RVKGRWTWLTGCTPEYLAP 198
QY 264 EVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVSQVMYENILHQPLQIPGGRTVAACD 323
Db 199 EILSKGYNKAVDWWALGVLIYEMAAGYPPFPADQIQIYEKIVSGKVRFPFSFSDLDK 258
QY 324 LLOSLLHKDQORLGS-KADFL-EIKNVFFSPINWDDLYHKRLTPFPNPNVTGPDADLKH 382
Db 259 LLRNLLQVLDLTKRFGNLKGVNDIKNHWKFWATTDTWIAIYQKVEAPFIPKFKGPGDTSNF 318

QY 383 DPEFTQEA VSKSI 395
Db 319 D-DYEEEEEIRVSI 330
RESULT 8
US-11-092-168-3
; Sequence 3, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bearss, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-092-168-3

Query Match 30.1%; Score 694.5; DB 7; Length 343;
Best Local Similarity 43.1%; Pred. No. 1.6e-51;
Matches 135; Conservative 66; Mismatches 105; Indels 7; Gaps 5;
QY 84 PSANPNAQPTDFDLKVIKGNVGVKLLAKRKS DGAFYAVKVLQKKSILKKKEQSHIMAE 143
Db 26 PAQN-TAHLDDQPERIKTLGTSGFGRVNLVKHKTGNHFAFKILDKQKVKLKQIEHTLNE 84
QY 144 RSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGELFFHLQRRRFLPRARFYAAEV 203
Db 85 KRI-LQAVNFPFLVKLEYSFKDNLNMYMVEYVPGGEMFSLRRIGRFSSEPHARFYAAQI 143
QY 204 ASAIGVLSLNIYRDLKPNILLDCQGHVLLTDGCLCKEGVEPDETTSTFCGTPPYLAP 263
Db 144 VLTFEYLSLDLIYRDLKPNILLDQGGYIQVTDFGFAK---RVKGRWTWLTGCTPEYLAP 200
QY 264 EVLRKEPYDRAVDWCLGAVLYEMLHGLPPFYSDVSQVMYENILHQPLQIPGGRTVAACD 323
Db 201 EILSKGYNKAVDWWALGVLIYEMAAGYPPFPADQIQIYEKIVSGKVRFPFSFSDLDK 260
QY 324 LLOSLLHKDQORLGSKADFL-EIKNVFFSPINWDDLYHKRLTPFPNPNVTGPDADLKH 382
Db 261 LLRNLLQVLDLTKRFGNLKGVNDIKNHWKFWATTDTWIAIYQKVEAPFIPKFKGPGDTSNF 320
QY 383 DPEFTQEA VSKSI 395
Db 321 D-DYEEEEEIRVSI 332
RESULT 9

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C;Genetics:
A;Gene: GDB:AKT3
A;Cross-references: GDB:9954867
A;Map position: 1q44-1q44
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;4-105/Domain: pleckstrin repeat homology <PLK>
F;146-405/Domain: protein kinase homology <KIN>
F;154-162/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted

Query Match 38.2%; Score 883.5; DB 1; Length 462;
Best Local Similarity 51.2%; Pred. No. 2.9e-34;
Matches 173; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

Qy 60 RMSSSPAGTSPQPSRAN--GNINLGSANPNNAOPT--DFDFLKVIKGNVGVKLLAKRK 115
Db 116 RMNCSPT-----SQIDNIGEEEMDASTTHHKRKTWNDFDLKLLGKGTGKVLVREK 168
Qy 116 SDGAFYAVKVLQKSKILKKKEQSHIMAEVSLLKNVHPFLVGLRYSFQTPKLYFVLDY 175
Db 169 ASGKYIAMKILKEVIAKDEVAHTLSE-SRVLNKTRHPFLTSUKYSFQTKDRLCFVMEY 227
Qy 176 VNGGELFFHLQRRERFLEPRARFYAAEVAISAIGVLSHLSNIYRDLPENILLDCQGHVVL 235
Db 228 VNGGELFFHLRSERVFSEDRTRFYGAIVSALDYVLSGKIVYRDLEMLDKDGHKI 287
Qy 236 TDFGLCKEGVEPEDTTSTFCGTPPYLAPEVLRKEPYDRAVDWVWCLGAVLYEMHLGLPPFY 295
Db 288 TDFGLCKEGITDAATMTKTCGTPPYLAPEVLENDYGRAVDWVWCLGVVYEMMCGRLPFY 347
Qy 296 SQDVSMYENILHQPLOIPGGRVVAACDLQLSLHKDQORQLGSKADFLKIKHNVFSP 354
Db 348 NQDHEKLFELIMEDIKFPRTLSSDAKSLSLGILLKDPNKRKLGSGPDDPKEIMRHSFSG 407
Qy 355 INWDDLYHKELTPFPNPNVTGPADLKHDPDEFTQEAVS 392
Db 408 VNWQDVYDKLVPPFKPQVTSQVTDTRYFDEEFTAQIT 445

RESULT 5
JC4345
protein kinase (EC 2.7.1.37) akt3 [validated] - rat
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C;Accession: J04345
R;Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K
Biochem. Biophys. Res. Commun. 216, 526-534, 1995
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase
e C subtypes and beta gamma subunits of G proteins.
A;Reference number: JC4345; MUID:96063640; PMID:7488143
A;Accession: J04345
A;Molecule type: mRNA
A;Residues: 1-454 <KON>
A;Cross-references: UNIPROT:Q63484; UNIPARC:UPI0000012577F; DDBJ:D49836; NID:g1136777; PI
A;Experimental source: brain
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;4-105/Domain: pleckstrin repeat homology <PLK>
F;146-405/Domain: protein kinase homology <KIN>
F;154-162/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted

Query Match 38.2%; Score 882.5; DB 1; Length 454;
Best Local Similarity 51.2%; Pred. No. 3.2e-34;
Matches 173; Conservative 53; Mismatches 99; Indels 13; Gaps 5;

Qy 60 RMSSSPAGTSPQPSRAN--GNINLGSANPNNAOPT--DFDFLKVIKGNVGVKLLAKRK 115
Db 116 RMNCSPT-----SQIDNIGEEEMDASTTHHKRKTWNDFDLKLLGKGTGKVLVREK 168
Qy 116 SDGAFYAVKVLQKSKILKKKEQSHIMAEVSLLKNVHPFLVGLRYSFQTPKLYFVLDY 175
Db 169 ASGKYIAMKILKEVIAKDEVAHTLSE-SRVLNKTRHPFLTSUKYSFQTKDRLCFVMEY 227
Qy 176 VNGGELFFHLQRRERFLEPRARFYAAEVAISAIGVLSHLSNIYRDLPENILLDCQGHVVL 235
Db 228 VNGGELFFHLRSERVFSEDRTRFYGAIVSALDYVLSGKIVYRDLEMLDKDGHKI 287
Qy 236 TDFGLCKEGVEPEDTTSTFCGTPPYLAPEVLRKEPYDRAVDWVWCLGAVLYEMHLGLPPFY 295
Db 288 TDFGLCKEGITDAATMTKTCGTPPYLAPEVLENDYGRAVDWVWCLGVVYEMMCGRLPFY 347
Qy 296 SQDVSMYENILHQPLOIPGGRVVAACDLQLSLHKDQORQLGSKADFLKIKHNVFSP 354
Db 348 NQDHEKLFELIMEDIKFPRTLSSDAKSLSLGILLKDPNKRKLGSGPDDPKEIMRHSFSG 407
Qy 355 INWDDLYHKELTPFPNPNVTGPADLKHDPDEFTQEAVS 392
Db 408 VNWQDVYDKLVPPFKPQVTSQVTDTRYFDEEFTAQIT 445

RESULT 6
S33364
protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: S33364
R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Teguchi, T.; Gardner,
Oncogene 8, 745-754, 1993
A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt
A;Reference number: S33364; MUID:93173519; PMID:8437858
A;Accession: S33364
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-480 <BEL>
A;Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PI
C;Genetics:
A;Gene: MGI:Akt
A;Cross-references: MGI:87986
A;Map position: 12
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 38.0%; Score 878.5; DB 1; Length 480;
Best Local Similarity 47.8%; Pred. No. 5.1e-34;
Matches 175; Conservative 58; Mismatches 102; Indels 31; Gaps 7;

Qy 66 AGTPSPQPSRANGNINLGSANPNNAOPT--DFDFLKVIKGNVGVKLLAKRKSDGAPYAV 123
Db 122 SGSPSPNSGAEMEVSLSL--AKPKHRTVMNEFEYLLKLGKGTGKVLVREKATGRYAM 178
Qy 124 KVLQKSKILKKKEQSHIMAEVSLLKNVHPFLVGLRYSFQTPKLYFVLDYVNGGSLFF 183
Db 179 KILKKEVIAKDEVAHTLTENRV-LQNSRHPFTALKYSFQTHDRLCFVMEYANGGLFF 237
Qy 184 HLQRRERFLEPRARFYAAEVAISAIGVLSHLSNIYRDLPENILLDCQGHVLTDFGLCK 242
Db 238 HLSRERVFSEDRARFYGAIVSALDYVLSGKIVYRDLEMLDKDGHKIITDFGLCK 297

QY 243 EGVPEPDTTSTFCGTPYLAPVLRKEPYDRAVDWMCIGAVLYEMHLGLPPFYSDVQSOM 302
DB 298 EGKKGATWKTCGTPYLAPVLRKEPYDRAVDWMCIGAVLYEMHLGLPPFYSDVQSOM 357
QY 303 YENILHQPLOIPGGRRTVAACDLQSLHKKDQORL--GSKADFLFIKNHVFFSPINWDDLY 361
DB 358 FELILMEEIRFPRTLGLPEAKSLLSGLLKKDPTQRLGGGSEDAKEIMQHRFFANIVWQDVI 417
QY 362 HKRLTPFPNPNVTGADLKHPDPEFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPED 421
DB 418 EKLSPPFPKQVTSSTDRYDFDEFTAQMIT-----ITP-----PDQ 454
QY 422 DDILDC 427
DB 455 DDSMEC 460
RESULT 7
A40831
gag-akt polypotein - AKT8 murine leukemia virus
N:Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin
C:Species: AKT8 murine leukemia virus
C:Date: 12-Feb-1993 #sequence_revision 12-May-1994 #text_change 31-Dec-2004
C:Accession: A40831, B40831
R:Bellocosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.
Science 254, 274-277, 1991
A:Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH
A:Reference number: A40831; MUID:92022574; PMID:1833819
A:Accession: A40831
A:Molecule type: DNA
A:Residues: 1-262 <BEL>
A:Cross-references: UNIPARC:UPI00001725AF; GB:M80675
A:Accession: B40831
A:Molecule type: DNA
A:Residues: 262-763 <BE2>
A:Cross-references: UNIPARC:UPI00001725B0; GB:M80675
C:Genetics:
A:Gene: gag-akt
C:Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferas
F:1-129/Product: core protein p15 #status predicted <CP1>
F:130-214/Product: inner coat protein p12 #status predicted <CP2>
F:284-763/Product: kinase-related transforming protein akt #status predicted <AKT>
F:287-389/Domain: pleckstrin repeat homology <PK>
F:431-691/Domain: protein kinase homology <KIN>
F:439-447/Region: protein kinase ATP-binding motif
F:25,337/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:462/Active site: Lys #status predicted
F:609/Binding site: phosphate (Tyr) (covalent) #status predicted
Query Match 38.0%; Score 878.5; DB 1; Length 763;
Best Local Similarity 47.8%; Pred. No. 7.7e-34;
Matches 175; Conservative 58; Mismatches 102; Indels 31; Gaps 7;
QY 66 ACTPSQPSRANGNINLGPANNAOPT--DFPLKVGKNGYKVLAKRKSDDGAFYAV 123
DB 405 SGSPNSNGSAEMEVSU---AKPKHRTVMNEFYLKLLGKGTGKVLVKEKATGRYAM 461
QY 124 KVLQKSLKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGELFF 183
DB 462 KILKEVIVAKDEVAHTLTENRV-LQNSRHFFLTALKYSFQTHDRLCFVMEYANGELFF 520
QY 184 HLQRRFLPRARFYAAEVAASIGYLS--LNIIYRDLKPNILDCQGHVLTDFGLCK 242
DB 521 HLSRERFVSDRARFYGAIEVSALDYHSEKNVVRDLKLENMLDKDGHIKITDFGLCK 580
QY 243 EGVPEPDTTSTFCGTPYLAPVLRKEPYDRAVDWMCIGAVLYEMHLGLPPFYSDVQSOM 302
DB 581 EGKKGATWKTCGTPYLAPVLRKEPYDRAVDWMCIGAVLYEMHLGLPPFYSDVQSOM 357
QY 303 YENILHQPLOIPGGRRTVAACDLQSLHKKDQORL--GSKADFLFIKNHVFFSPINWDDLY 361
DB 641 FELILMEEIRFPRTLGLPEAKSLLSGLLKKDPTQRLGGGSEDAKEIMQHRFFANIVWQDVI 700

QY 362 HKRLTPPRPNVNTGADLKHPDPEFTQEAIVSKSIGCTPDTVASSSGASSAFLGFSYAPED 421
DB 701 EKLSPPFPKQVTSSTDRYDFDEFTAQMIT-----ITP-----PDQ 737
QY 422 DDILDC 427
DB 738 DDSMEC 743
RESULT 8
A46288
protein kinase (EC 2.7.1.37) akt2 - human
N:Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protei
C:Species: Homo sapiens (man)
C:Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
C:Accession: A46288
R:Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.;
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992
A:Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/thr
A:Reference number: A46288; MUID:93028445; PMID:1409633
A:Accession: A46288
A:Molecule type: mRNA
A:Residues: 1-481 <CHE>
A:Cross-references: UNIPROT:P31751; UNIPARC:UPI000049EDB; GB:M95936; NID:G178325; PIDN
A:Note: sequence extracted from NCBI backbone (NCBIP:115859)
C:Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.
C:Genetics:
A:Gene: GDB:AKT2
A:Cross-references: GDB:135660; OMIM:164731
A:Map position: 19q13.2-19q13.2
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
F:4-106/Domain: pleckstrin repeat homology <PK>
F:150-409/Domain: protein kinase homology <KIN>
F:158-166/Region: protein kinase ATP-binding motif
F:181/Active site: Lys #status predicted
Query Match 37.9%; Score 876; DB 1; Length 481;
Best Local Similarity 48.9%; Pred. No. 6.7e-34;
Matches 174; Conservative 57; Mismatches 113; Indels 12; Gaps 5;
QY 70 SPQPSRANGNINLGPANNAOPTDFPLKVGKNGYKVLAKRKSDDGAFYAVKVLQK 128
DB 126 SPDSSTTEEMEVAIVSKAKAKVTMDFYLLKLGKGTGKVLVREKATGRYAMKILRK 185
QY 129 KSILKKQSHIMAERSVLLKNVRHPFLVGLRYSFQTPKLYFVLDYVNGGELFFHLORE 188
DB 186 EVIIAKDEVAHTVTE--SRVLQNRHPFLTALKYAFQTHDRLCFVMEYANGELFFHLSRE 244
QY 189 RFLPLPRARFYAAEVAASIGYLSNIIYRDLKPNILDCQGHVLTDFGLCKEGVEPE 248
DB 245 RVFTTERARFYGAIEVSALDYHSEKNVVRDLKLENMLDKDGHIKITDFGLCKEGISDG 304
QY 249 DTTSTFCGTPYLAPVLRKEPYDRAVDWMCIGAVLYEMHLGLPPFYSDVQSOMYENILH 308
DB 305 ATMTKFCGTPYLAPVLRKEPYDRAVDWMCIGAVLYEMHLGLPPFYSDVQSOMYENILH 364
QY 309 QELQIPGGRRTVAACDLQSLHKKDQORL--GSKADFLFIKNHVFFSPINWDDLYHKLTP 367
DB 365 BEIRFRTLSPKASLLAGLKKDKPKQLGGGSDAKEVMEHRFFLUSINWQDVVQKKLLP 424
QY 368 PENPNVTGADLKHPDPEFTQEAIVSKSIGCTPDTVASSSG-----ASSAFLGFSYA 418
DB 425 PFKPQVTSVDRYDFDEFT-----AQSIITTPDRYDLSGLLELDQTHPPQFSYS 476
RESULT 9
JC2437
protein kinase (EC 2.7.1.37) akt1 [validated] - rat

Db 238 HLSRERVSFSDRARFYGAETVSALDYLHSEKNVVYRDCLKLENMLDKDGHKIDTFLGLCK 297

QY 243 EGVEPEDTTSFTCGTPEYLAPEVLKPEYDRAVDWMLGAVLYEMLHGLPPFPYSQDVSQM 302

Db 298 EGIKDGATMKTFTCGTPEYLAPEVLEDNDYGRAVDWMLGAVLYEMLHGLPPFPYNQDHEKL 357

QY 303 YENILHQPLQIPGGRVTVAACDLLOSLHKKQORL-GSKADFLEIKNHVFFSPINWDDLY 361

Db 358 FELIMEEIRFPRTLPEAKSLSLGLKKDPKQRLGGSGSEDAKEIMQHRFFAGIVQHWY 417

QY 362 HKRLTPPFNNVTPGADLKHFDPEFTOEAVSKSIGCTGTPDTVASSSGASSAFLGFSVAPED 421

Db 418 EKLSPPFPKQVTSSETDTRIFDEFTQAQMIT---ITP-----PDQ 454

QY 422 DDLDC 427

Db 455 DDSMEC 460

RESULT 11

S37955

protein kinase YPK1 (EC 2.7.1.1-) - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein YKL126w

C;Species: Saccharomyces cerevisiae

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Oct-2004

C;Accession: S37955; A31248; S30903

R;Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P. submitted to the Protein Sequence Database, March 1994

A;Reference number: S37953

A;Accession: S37955

A;Molecule type: DNA

A;Residues: 1-680 <RAM>

A;Cross-references: UNIPROT:P12688; UNIPARC:UPI0000113BDF5; EMBL:Z28126; NID:G486212; PID:R;Maurer, R.A.

A;Experimental source: strain S288C

DNA 7, 469-474, 1988

A;Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein

A;Reference number: A31248; MUID:89090805; PMID:2850145

A;Accession: A31248

A;Molecule type: DNA

A;Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>

A;Cross-references: UNIPARC:UPI0000168D89; EMBL:M21307; NID:g172180; PIDN:AAA34880.1; PI

R;Chen, P.; Lee, K.S.; Levin, D.E.

Mol. Gen. Genet. 236, 443-447, 1993

A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell gr

A;Reference number: S30903; MUID:93173125; PMID:8437590

A;Accession: S30903

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>

A;Cross-references: UNIPARC:UPI000017A451

C;Genetics:

A;Gene: SGD:YPK1

A;Cross-references: SGD:S0001609; MIPS:YKL126w

A;Map position: 11L

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F;345-602/Domain: protein kinase homology <KIN>

F;353-361/Region: protein kinase ATP-binding motif

F;470/Active site: Asp #status predicted

Query Match 37.5%; Score 866; DB 2; Length 680;

Best Local Similarity 51.5%; Pred. No. 2.6e-33;

Matches 177; Conservative 53; Mismatches 106; Indels 8; Gaps 5;

QY 75 RANGNINLGPANPNQAQPTDFDLKVIKGNKYKLLAKKSDGAFVAVKVLQKKSILKK 134

Db 327 KINISIDYKSRNKPISIDDFDLKVIKGSFGKVMQVRKQTKQYALKAKRKSIYVK 386

QY 135 KEOSHIMAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLVDYVNGBELFFHLQRRERFLPE 194

Db 387 SEVTHTLAERTVLAR-VDCPFIVPLKFSFQSPKLYFVLAFINGGELFYHLQKEGRFDLS 445

QY 195 RARFYAAEVASATGYLHSLNIYRDCLKPENILDCQGHVVLTDFGLCKSGVEEDTITSF 254

Db 446 RARFYAEILCALDNLHKLVDVYRDCLKPENILDDVQHIALCDFGLCKLNMKDDDKTDTF 505

QY 255 CQTPEYLAPEVLKPEYDRAVDWMLGAVLYEMLHGLPPFPYSQDVSMYENILHQPLQIP 314

Db 506 CQTPEYLAPELLGLGYTKAVDWTGLVLLYEMLTGLPEYDEDVPKMYKKILQEPLVFP 565

QY 315 GGRTVAAACDLLQSLHKKQORLG-SKADFLEIKNHVFFSPINWDDLYHKRLTTPPNPV 373

Db 566 DGFDRDAKDLGLLGRDPTRLRYNGAD--BIRNHPFESQLSWKRLLMKGYIPPYKPAV 623

QY 374 TGPADLKHFDPEFTOEAVSKSIGCTGTPDTVASSSGASSAFLGFSY 417

Db 624 SNSMDSNFDEFTRE---KPIDSVVDEYLSSES-VQKQFGGWTY 663

RESULT 12

S62117

protein kinase (EC 2.7.1.1.37) akt1 [similarity] - bovine

N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prot.

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004

C;Accession: S62117; S24423; S17999; S15714; S36388

R;Coffer, P.J.; Woodgett, J.R. submitted to the EMBL Data Library, December 1991

A;Reference number: S62117

A;Accession: S62117

A;Molecule type: mRNA

A;Residues: 1-480 <COF>

A;Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:g630; PIDN:R;Coffer, P.J.; Woodgett, J.R.

A;Note: this is a revision to the sequence from reference S17999

Eur. J. Biochem. 205, 1217, 1992

A;Reference number: S24423; MUID:92249329; PMID:1533586

A;Contents: erratum

A;Accession: S24423

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 70-78, 'N', 80-145 <COW>

A;Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036

A;Note: this is a revision to the sequence from reference S17999

R;Coffer, P.J.; Woodgett, J.R.

Eur. J. Biochem. 201, 475-481, 1991

A;Title: Molecular cloning and characterisation of a novel putative protein-serine kina

A;Reference number: S17999; MUID:92037600; PMID:1718748

A;Accession: S17999

A;Molecule type: mRNA

A;Residues: 1-70, 'TPSSSAACGPRSSSARSTRPRSGVGVDRHRPDGRRQAEGGDDGLPVGLTRRELGGRGGVAGQ

A;Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036

A;Note: this sequence has been revised in references S62117 and S24423

C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni

A;Pathway: signal transduction pathways regulating various processes

C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen

F;4-106/Domain: pleckstrin repeat homology <PLK>

F;148-408/Domain: protein kinase homology <KIN>

F;156-164/Region: protein kinase ATP-binding motif

F;179/Active site: Lys #status predicted

F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k-

F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 37.4%; Score 863.5; DB 1; Length 480;

Best Local Similarity 48.2%; Pred. No. 2.5e-33;

Matches 174; Conservative 60; Mismatches 112; Indels 15; Gaps 7;

QY 66 AGTPSPQPSRANGNINLGPANPNQAQPT--DFDFLKVIKGNKYKLLAKKSDGAFYAV 123

Db 122 SGSPGNGSAEEMEYSL---AKPKGRVTNNEFYKLLKGLKGTGKVLVKKKATAAYAM 178

QY 124 KYVLQKKSLKKKEQSHIMAERSVLLKNVRHPLVGLRYSFQTPEKLYFVLVDYVNGGELFF 183

Db 179 KILKKEIVAKDEVAHTLTENRV-LQNSRHPSLTALKYSFQTHDRILCFWMEYANGGELFF 237

A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell growth
A;Reference number: S30903; MUID:93173125; PMID:8437590
A;Accession: S30904
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-677 <CHE>
A;Cross-references: UNIPARC:UPI000013BDFF
R;Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54510
A;Accession: S54565
A;Molecule type: DNA
A;Residues: 1-677 <HUN>
A;Cross-references: UNIPARC:UPI000013BDFF; EMBL:Z49702; NID:9817859; PIDN:CAA89740.1; PT
C;Genetics:
A;Gene: SGD:YPK2; YKR2
A;Cross-references: SGD:S0004710; MIPS:YMR104C
A;Map position: 13R
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;35-57/Region: histidine-rich
F;342-599/Domain: protein kinase homology <KIN>
F;350-358/Region: protein kinase ATP-binding motif
F;351-375/Region: ATP binding #status predicted
F;466-512/Region: catalytic #status predicted

Query Match 36.6%; Score 846; DB 2; Length 677;
Best Local Similarity 49.9%; Pred. No. 2.2e-32;
Matches 175; Conservative 50; Mismatches 116; Indels 10; Gaps 5;

Qy	75	RANGINL----	GPSANPNAQPTDFDLKVIKGNVCKVLLAKRKS	SDGAFYAVKVLQKKS	130
Db	320	RGYKGLNITVDYKPSKNKPLSIDDFDLKVIKGSFGKQVNRKKTQKIYALKLRKAY	379		
Qy	131	ILKKKEQSHIMASRSLKNNRHPFLVGLRYSQTPEKLYFLVDYVNGGELFPHLQERR	190		
Db	380	IVSKCEVTHLAERTVLAR-VDCFFIVPLKFSQSEKLYLVLAFLNGGELFYHLOEGR	438		
Qy	191	FLEPRARFYAAEVASAIQYHLSNIYRDLKPENILLDQGHVVLTDGLCKEGVPEPT	250		
Db	439	FSLARSFYTAELLCALDSLKLKLDVIYRDLKPENILLDYQGHIALCDFGLCKLNMKDNK	498		
Qy	251	TSTPCGTPEYLAPEVLRKEPYDRAVDWMCIGAVLYEMLHGLPPFYSDYVSQMYENILHQP	310		
Db	499	TDTFCGTPEYLAPEILLGQGYTKTVDMWTGLILLYEMMTGLPPYDENVPMYKILQQP	558		
Qy	311	LQIPGGRTVAACDLLOSLHKQORLGSKADFLKKNHVFSPINWDDLYHKRLTPPFN	370		
Db	559	LLFPDGFDPAAKDLLLGLLSRDPSSRLGVNGTD-EIRNHPFFKDISWKKLLKGYIPPYK	617		
Qy	371	PNVTGPADLKHDPFTQEAIVSKSIGCTPDTVASSGASSAFIGFSYAPED	421		
Db	618	PIVKSEIDTANFDQETKE---KPIDSVVDVDEYLSAS-IQKQFGGWTYIGDE	664		

Search completed: January 27, 2006, 23:32:06
Job time : 13.622 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2006, 23:08:15 ; Search time 69.5554 Seconds
(without alignments)
4331.236 Million cell updates/sec

Title: US-09-868-131A-8
Perfect score: 2311
Sequence: 1 MQGLLTSGRKPSGGGRCTGR.....ASSAFLGSVAPEDDDILD 427

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	100.0	427	1	SGK2 HUMAN
2	2311	100.0	427	2	Q5H8Y6 HUMAN
3	2064	89.3	393	2	Q52PK5 HUMAN
4	1947	84.2	367	2	Q5T2R3 HUMAN
5	1938.5	83.9	366	2	Q5H821 HUMAN
6	1932	83.6	367	2	Q5RD29_PONPY
7	1848	80.0	367	1	SGK2 MOUSE
8	1540	66.6	302	1	SGK2 RAT
9	1497	64.8	285	2	Q5H8Y4 HUMAN
10	1450.5	62.8	350	2	Q4S7V9_TETNG
11	1445.5	62.5	431	2	Q5Q0U5_FUNHE
12	1440.5	62.3	433	2	Q7ZTW4_BRARE
13	1427	61.7	432	2	Q6UI19_CHICK
14	1425.5	61.7	434	2	Q93524_XENLA
15	1423	61.6	431	1	SGK1 RABIT
16	1422.5	61.6	434	2	Q6GPN6_XENLA
17	1420	61.4	431	2	Q68G05_RAT
18	1419	61.4	421	1	Q5TCN4 HUMAN
19	1419	61.4	431	2	Q5TCN3 HUMAN
20	1419	61.4	445	2	Q5TCN2 HUMAN
21	1419	61.4	526	2	Q5V765 HUMAN
22	1418.5	61.4	418	2	Q5BKX4_XENTR
23	1416	61.3	431	1	SGK3 MOUSE
24	1416	61.3	519	2	Q6NS85_MOUSE
25	1415	61.2	431	1	SGK1 HUMAN
26	1414	61.2	431	2	Q4R633_MACFA
27	1411.5	61.1	430	1	SGK1 RAT
28	1404.5	60.8	490	2	Q4RR91_TETNG
29	1399	60.5	434	2	Q6GLY8_XENLA
30	1392	60.2	594	2	Q73927_SQUAC
31	1390.5	60.2	433	2	Q73926_SQUALUS

32	1338.5	57.9	429	2	Q8VEK1_MOUSE
33	1338.5	57.9	496	1	SGK3_MOUSE
34	1328.5	57.5	429	2	Q6FHV7_HUMAN
35	1328.5	57.5	496	1	SGK3_HUMAN
36	1328.5	57.5	496	2	Q53EW6_HUMAN
37	1328.5	57.5	496	2	Q5R7A7_PONPY
38	1323.5	57.1	496	2	Q5H9Q5_HUMAN
39	1320.5	57.1	518	2	Q4SFC2_TETNG
40	1319.5	57.1	490	2	Q5ZJQ4_CHICK
41	1213	52.5	1114	2	Q4SVX7_TETNG
42	1063	46.0	316	2	Q4RI65_TETNG
43	1035	44.8	1550	2	Q4SIY0_TETNG
44	1025.5	44.4	198	2	Q5H8Y5_HUMAN
45	984	42.6	423	2	Q613H2_CAEBR

ALIGNMENTS

RESULT 1
SGK2 HUMAN
ID_SGK2_HUMAN STANDARD; PRT; 427 AA.
AC Q9HY8; Q9UKG6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2).
GN Name=SGK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), PHOSPHORYLATION SITE THR-253,
RP AND MUTAGENESIS OF SER-416.
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021:3440189;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).

[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 1).
MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RX Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lenvaestaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McMay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rameay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain, and Colon;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; JGI
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION.
RX MEDLINE=22284526; PubMed=12397388; DOI=10.1007/s00424-002-0873-2;
RA Gamber N., Fillon S., Feng Y., Friedrich B., Lang P.A., Henke G.,
RA Huber S.M., Kobayashi T., Cohen P., Lang F.;
RT "K(+) channel activation by all three isoforms of serum- and
RT glucocorticoid-dependent protein kinase SGK.";
RL Pflugers Arch. 445:60-66(2002).
CC -!- FUNCTION: Involved in the activation of potassium channels.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2; Synonyms=beta;
CC IsoId=Q9HBY8-1; Sequence=Displayed;
CC Name=1; Synonyms=alpha;
CC IsoId=Q9HBY8-2; Sequence=VSP_004932;
CC -!- TISSUE SPECIFICITY: Highly expressed in liver, kidney and
CC pancreas, and at lower levels in brain.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: Not regulated by serum or glucocorticoids.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC ENBL; AF186470; AAG17012.1; -; mRNA.
CC ENBL; AF169034; AAF12757.2; -; mRNA.
CC ENBL; Z98752; CAC18509.1; -; Genomic DNA.
CC ENBL; BC014037; AAH14037.2; ALT SEQ; mRNA.
CC ENBL; BC065511; AAH65511.1; -; mRNA.
CC HSSP; P31751; 1GZK.
CC Ensembl; ENSG00000101049; Homo sapiens.
CC HGNC; HGNC:13900; SGK2.
CC MIM; 607589; -;
CC GO; GO:0015459; F:potassium channel regulator activity; IDA.
CC GO; GO:0004682; F:protein kinase CK2 activity; NAS.
CC GO; GO:0004874; F:protein serine/threonine kinase activity; TAS.
CC GO; GO:0017080; F:sodium channel regulator activity; NAS.
CC GO; GO:0004688; F:protein amino acid phosphorylation; NAS.
CC GO; GO:0007243; P:protein kinase cascade; TAS.
CC GO; GO:0006979; P:response to oxidative stress; TAS.
CC InterPro; IPR000961; Pkinase.C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_Thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00433; Pkinase C; 1.
CC ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 95 352 Protein kinase.
FT NP_BIND 101 109 ATP (By similarity).
FT MOTIF 128 138 Nuclear localization signal (By similarity).
FT ACT_SITE 219 219 Proton acceptor (By similarity).
FT BINDING 124 124 ATP (By similarity).
FT MOD_RES 253 253 Phosphothreonine (By PPK1).
FT VARSPPLIC 1 60 Missing (in isoform 1).
FT FTID=VSP_004932.
FT MUTAGEN 416 416 S->D: Increased activation.
SQ SEQUENCE 427 AA; 47604 MW; D8FOFA6DF54B1370 CRC64;
Query Match 100.0%; Score 2311; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.2e-145;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOGLLTSGRKPSGGGRCCTGCGWGWCLKPMWGGADPTPTLSCLLLPVPPELPDHCYR 60
DB 1 MOGLLTSGRKPSGGGRCCTGCGWGWCLKPMWGGADPTPTLSCLLLPVPPELPDHCYR 60
QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVLAKRKS DGAF 120
DB 61 MNSSPAGTSPQPSRANGNINLGPSANPNAQPTDFDLKVIKGNYGKVLAKRKS DGAF 120
QY 121 YAVVLQKKSILKKKEQSHIMERSVLLKNVHPFLVGLRYSFQTPKLYFVLDDYNGGE 180
DB 121 YAVVLQKKSILKKKEQSHIMERSVLLKNVHPFLVGLRYSFQTPKLYFVLDDYNGGE 180
QY 181 LFFHLQRRERFLEPRARFYAAEVASVAGIYHLSNIIYRDLKPNILLDCQGHVLLTDFGL 240
DB 181 LFFHLQRRERFLEPRARFYAAEVASVAGIYHLSNIIYRDLKPNILLDCQGHVLLTDFGL 240
QY 241 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPFYSDVS 300
DB 241 CKEGVEPEDTTSTFCGTPPEYLAPEVLKPEPYDRAVDMWCLGAVLYEMLHGLPFYSDVS 300
QY 301 QMYENILHQPLOIPGGRITVAACDLQSLHKKQRLGSKADFLKKNHVFSPINWDDL 360
DB 301 QMYENILHQPLOIPGGRITVAACDLQSLHKKQRLGSKADFLKKNHVFSPINWDDL 360
QY 361 YHKRLTPPPNPVNTGPDALKHFDPEPTQBAVSKSIGCTPDTVASSSGASSAFGLFSYAPE 420
DB 361 YHKRLTPPPNPVNTGPDALKHFDPEPTQBAVSKSIGCTPDTVASSSGASSAFGLFSYAPE 420
RESULT 2
Q5H8Y6 HUMAN
ID Q5H8Y6 HUMAN PRELIMINARY; PRT; 427 AA.
AC Q5H8Y6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE OTTHUMP00000031703.
GN Name=SGK2; ORFNames=RP1-138B7.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Beasley H.;

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RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z98752; CA142312.1; -; Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 427 AA; 47604 MW; D8F0FA6DF54B1370 CRC64;

Query Match 100.0%; Score 2311; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.2e-145;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQGLLTSGRKPSGGGRCCTGRGGWRGQWCLKPMWGGADPPTTSLCLLLPVPELPDHCYR 60
DB 1 MQGLLTSGRKPSGGGRCCTGRGGWRGQWCLKPMWGGADPPTTSLCLLLPVPELPDHCYR 60
QY 61 MNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKVIGKNGYKVLAKRKSQDGF 120
DB 61 MNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKVIGKNGYKVLAKRKSQDGF 120
QY 121 YAVKVLQKSLKKKQSHIMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLDDYNGGE 180
DB 121 YAVKVLQKSLKKKQSHIMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLDDYNGGE 180
QY 181 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNILLDCQGHVLTDFGL 240
DB 181 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNILLDCQGHVLTDFGL 240
QY 241 CKGEVPEPDTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCILGAVLYEMLHGLPPFYSQDVS 300
DB 241 CKGEVPEPDTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCILGAVLYEMLHGLPPFYSQDVS 300
QY 301 QMYENILHQLPIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINHVFFSPINWDDL 360
DB 301 QMYENILHQLPIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINHVFFSPINWDDL 360
QY 361 YHKRLTPFPNPNVTGPADLKHFDPFTQEAHSVKSIGCTPDTVAASSGASSAFGLGFSVAPE 420
DB 361 YHKRLTPFPNPNVTGPADLKHFDPFTQEAHSVKSIGCTPDTVAASSGASSAFGLGFSVAPE 420
QY 421 DDILDC 427
DB 421 DDILDC 427

RESULT 3
Q52PK5 HUMAN PRELIMINARY; PRT; 393 AA.
AC Q52PK5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serum/glucocorticoid regulated kinase 2.
GN Name-SGK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RA Li H., Nong W., Zhou G., Ke R., Shen C., Zhong G., Zheng Z., Liang M.,
RA Xiao W., Lin L., Yang S.;
RT "Direct Submission.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY987010; AAX88805.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 393 AA; 43962 MW; B9931E71A8B998D6 CRC64;

Query Match 89.3%; Score 2064; DB 2; Length 393;
Best Local Similarity 91.6%; Pred. No. 7.3e-129;
Matches 391; Conservative 1; Mismatches 1; Indels 34; Gaps 1;

QY 1 MQGLLTSGRKPSGGGRCCTGRGGWRGQWCLKPMWGGADPPTTSLCLLLPVPELPDHCYR 60
DB 1 MQGLLTSGRKPSGGGRCCTGRGGWRGQWCLKPMWGGADPPTTSLCLLLPVPELPDHCYR 26
QY 61 MNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKVIGKNGYKVLAKRKSQDGF 120
DB 27 MNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKVIGKNGYKVLAKRKSQDGF 86
QY 121 YAVKVLQKSLKKKQSHIMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLDDYNGGE 180
DB 87 YAVKVLQKSLKKKQSHIMAERSVLLKNVRPFLVGLRYSQTPEKLYFVLDDYNGGE 146
QY 181 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNILLDCQGHVLTDFGL 240
DB 147 LFPHLQRRERFLPRARFYAAEVAASAIYGLHLSNIIYRDLKPNILLDCQGHVLTDFGL 206
QY 241 CKGEVPEPDTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCILGAVLYEMLHGLPPFYSQDVS 300
DB 207 CKGEVPEPDTTSTFCGTPPEYLAPEVLKPEPYDRAVDWMCILGAVLYEMLHGLPPFYSQDVS 266
QY 301 QMYENILHQLPIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINHVFFSPINWDDL 360
DB 267 QMYENILHQLPIPGGRTVAACDLLOSLLHKQORQLGSKADFLKINHVFFSPINWDDL 326
QY 361 YHKRLTPFPNPNVTGPADLKHFDPFTQEAHSVKSIGCTPDTVAASSGASSAFGLGFSVAPE 420
DB 327 YHKRLTPFPNPNVTGPADLKHFDPFTQEAHSVKSIGCTPDTVAASSGASSAFGLGFSVAPE 386
QY 421 DDILDC 427
DB 387 DDILDC 393

RESULT 4
Q52ZR3 HUMAN PRELIMINARY; PRT; 367 AA.
AC Q52ZR3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serum/glucocorticoid regulated kinase 2.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Kounindya M., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Phelan M., Farmer A.;
RA "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector."
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT020098; AA038901.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 367 AA; 41233 MW; C91DD892C4C2486B CRC64;

Query Match 84.2%; Score 1947; DB 2; Length 367;
Best Local Similarity 99.7%; Pred. No. 3.9e-121;
Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 120
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 60

QY 121 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 180
DB 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 120

QY 181 LFFHLQRRERFLPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240
DB 121 LFFHLQRRERFLPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 180

QY 241 CKEGVEPEDTTTFCGTPEYLAPEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSQDVS 300
DB 181 CKEGVEPEDTTTFCGTPEYLAPEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSQDVS 240

QY 301 QMYENILHQPLOIPGERTVAACDLQSLHKKQORLGSKADFLKKNHVFSPINWDDL 360
DB 241 QMYENILHQPLOIPGERTVAACDLQSLHKKQORLGSKADFLKKNHVFSPINWDDL 300

QY 361 YHKRLTPFPNPNVTGPADLKHDFPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
DB 301 YHKRLTPFPNPNVTGPADLKHDFPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 360

QY 421 DDILDC 427
DB 361 DDILDC 367

RESULT 5
QSH8Z1_HUMAN
ID QSH8Z1_HUMAN PRELIMINARY; PRT; 366 AA.
AC QSH8Z1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE OTTHUMP00000031706.
GN Name=SGK2; ORFNames=RP1-138B7.2-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z98752; CA142315.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 366 AA; 41047 MW; 8B8546894C23571F CRC64;

Query Match 83.9%; Score 1938.5; DB 2; Length 366;
Best Local Similarity 99.7%; Pred. No. 1.4e-120;
Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 120
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNNAQPTDFDLKVIKGNVGVLLAKRKS DGAF 60

QY 121 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 180
DB 61 YAVKVLQKKSILKKKEQSHIMAEVSLLKNVRHPELVGLRYSFQTPEKLYFVLDYVNGGE 119

QY 181 LFFHLQRRERFLPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 240
DB 120 LFFHLQRRERFLPRARFYAAEVAASIGYLHSLNIIYRDLKPENILLDCQGHVLTDFGL 179

QY 241 CKEGVEPEDTTTFCGTPEYLAPEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSQDVS 300
DB 180 CKEGVEPEDTTTFCGTPEYLAPEVLRKEPYDRAVDWVWCLGAVLYEMLHGLPPFYSQDVS 239

QY 301 QMYENILHQPLOIPGERTVAACDLQSLHKKQORLGSKADFLKKNHVFSPINWDDL 360
DB 240 QMYENILHQPLOIPGERTVAACDLQSLHKKQORLGSKADFLKKNHVFSPINWDDL 299

QY 361 YHKRLTPFPNPNVTGPADLKHDFPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 420
DB 300 YHKRLTPFPNPNVTGPADLKHDFPEFTQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPE 359

QY 421 DDILDC 427
DB 360 DDILDC 366

RESULT 6
QSRDZ9_PONPY
ID QSRDZ9_PONPY PRELIMINARY; PRT; 367 AA.
AC QSRDZ9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Hypothetical protein DKFZp469N2435.
GN Name=DKFZp469N2435;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Oeinger A., Pobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857741; CAH90008.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000433; Pkinase C; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein.
SQ SEQUENCE 367 AA; 41218 MW; 61128B6CC0519B73 CRC64;

Query Match 1 83.6%; Score 1932; DB 2; Length 367;
Best Local Similarity 98.6%; Pred. No. 3.9e-120;
Matches 362; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 61 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFLKVIGKNGVKVLLAKRKSQDGF 120
DB 1 MNSSPAGTSPQPSRANGNINLGPSANPNARPTDFLKVIGKNGVKVLLAKRKSQDGF 60

QY 121 YAVKVLQKSLKKSQSHIMARSVLLKNVRHFFLVGLRYSFQTEKLYFVLDVYNGGE 180
DB 61 YAVKVLQKSLKKSQSHIMARSVLLKNVRHFFLVGLRYSFQTEKLYFVLDVYNGGE 120

QY 181 LPFHLQRRRFLPRARFYAAEVAASIGYLHSLNIIVRDLPENILLDCQGHVLTDFGL 240
DB 121 LPFHLQRRRFLPRARFYAAEVAASIGYLHSLNIIVRDLPENILLDCQGHVLTDFGL 180

QY 241 CKGVSPEDTSTFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 300
DB 181 CKGVSPEDTSTFCGTPEYLAPEVLKPEYDRAVDWMCGLGAVLYEMLHGLPPFYSDVS 240

QY 301 QMVENILHQLQIPGGRITVAACDLQSLHKKQORLQSGKADFLKKNHVFSPINWDDL 360
DB 241 QMVENILHQLQIPGGRITVAACDLQSLHKKQORLQSGKADFLKKNHVFSPINWDDL 300

QY 361 YHKRLTPFPNPNVTPGADLKHDFEFTQEAIVSKSIGCTPDTVASSGASSAFLGFSYAPE 420
DB 301 YHKRLTPFPNPNVTPGADLKHDFEFTQEAIVSKSIGCTPDTVASSGASSAFLGFSYAPE 360

QY 421 DDDILDC 427
DB 361 DDDILDC 367

RESULT 7
SGK2_MOUSE
ID SGK2_MOUSE STANDARD; PRT; 367 AA.
AC Q9QZ85; Q8R0P6;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2).
GN Name=Sgk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=20018032; PubMed=10548550; DOI=10.1042/0264-6021.3440189;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schorbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wegner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiroaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in the activation of potassium channels (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9QZS5-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9QZS5-2; Sequence=VSP_004933;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: Not regulated by serum or glucocorticoids.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF169033; AAF12756.1; -; mRNA.
CC EMBL; AK050009; BAC34031.1; -; mRNA.
CC EMBL; BC026549; AAH26549.1; -; mRNA.
CC HSSP; P31751; IGZK.
CC Ensembl; ENSMUSG0000017868; Mus musculus.
CC MGI; MGI:135138; Sgk2.
CC GO; GO:0015459; F:potassium channel regulator activity; ISS.
CC GO; GO:0004682; F:protein kinase CK2 activity; ISS.
CC GO; GO:0017080; F:sodium channel regulator activity; ISS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase_I.
CC Pfam; PF00433; Pkinase_C; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TK; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 35 292
FT NP_BIND 41 49 ATP (By similarity).
FT MOTIF 68 78 Nuclear localization signal (By
FT similarity).
FT ACT_SITE 159 159 Proton acceptor (By similarity).
FT BINDING 64 64 ATP (By similarity).
FT MOD_RES 193 193 Phosphothreonine (by PDPK1) (By
FT similarity).
FT VARSPLIC 171 199 Missing (in isoform 2).
FT CONFLICT 77 77 /FTId=VSP_004933.3.
FT SEQUENCE 367 AA; 41359 MW; 668C04B1AE9E33A CRC64;
Query Match 80.0%; Score 1848; DB 1; Length 367;
Best Local Similarity 94.3%; Pred. No. 1.5e-114;
Matches 345; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 61 MNSSPAGTPSPQSRANGNTNLGSPANPNAPTDFDLKLVIGKNGYGVLLAKRKSDGAF 120
Db 1 MASSPVGVPSQPSRANGNTNLGSPANPNAPTDFDLKLVIGKNGYGVLLAKRKSDGAF 60
QY 121 YAVKVLQKSIILKKQESHIMAEBSVLLKNVRPFLVGLRYSQTPEKLYFVLVDYNGGE 180
Db 61 YAVKVLQKSIILKKQESHIMAEBSVLLKNVRPFLVGLRYSQTPEKLYFVLVDYNGGE 120
QY 181 LFPHLQRRERFLEPRARFYAAEVASAIGLYHLSNIYRDLKPNILLDCQGHVLTDFGL 240
Db 121 LFPHLQRRERFLEPRARFYAAEVASAIGLYHLSNIYRDLKPNILLDCQGHVLTDFGL 180
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QY 241 CKEGVEPEPTTSTFCGTPEYLAPEVLVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFYSDVVS 300
Db 181 CKECVEPEPTTSTFCGTPEYLAPEVLVRKEPYDRAVDWMCGLGAVLYEMLHGLPPFFNTDVA 240
QY 301 QMVENILHQPLOI PGGRITVAACDLQLSLHKQORQLGSKADFLFIKNHVFFSPINWDDL 360
Db 241 QMVENILHQPLOI PGGRITVAACDLQLSLHKQORQLGSKEDFLDKNHVFFSPINWDDL 300
QY 361 YHKRLTPPENPNVTGTPADLKHFDPEFTQBAVSKSGICTPDTVASSSGASSAFILGFSYAPE 420
Db 301 YHKRLTPPENPNVEGPAADLKHFDPEFTQBAVSKSGICTPDTVASSSGASSAFILGFSYAQD 360
QY 421 DDDILD 426
Db 361 DDDILD 366
RESULT 8
SGK2_RAT STANDARD; PRT; 302 AA.
AC Q8R4U9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase Sgk2 (EC 2.7.1.37)
DE (Serum/glucocorticoid regulated kinase 2) (Fragment).
DE Name=Sgk2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Feng Y.X., Huber S.M., Waerntges S., Lang F.;
RT "SGK2 and SGK3 mRNA expression in rat kidney.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the activation of potassium channels (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF361756; AAL91351.1; -; mRNA.
CC HSSP; P31751; IGZK.
CC Ensembl; ENSRNOG0000033573; Rattus norvegicus.
CC RGD; 620232; Sgk2.
CC GO; GO:0015459; F:potassium channel regulator activity; ISS.
CC GO; GO:0004682; F:protein kinase CK2 activity; ISS.
CC GO; GO:0017080; F:sodium channel regulator activity; ISS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TK; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 18 275
FT NP_BIND 24 32 ATP (By similarity).
FT MOTIF 51 61 Nuclear localization signal (By
FT similarity).
```

FT ACT_SITE 142 142 Proton acceptor (By similarity).
FT BINDING 47 47 ATP (By similarity).
FT MOD_RES 176 176 Phosphothreonine (by PDPK1) (By
FT similarity).
FT NON_TER 1 1
FT NON_TER 302 302
SQ SEQUENCE 302 AA; 34622 MW; A74EE3F424283D66 CRC64;
Query Match 66.6%; Score 1540; DB 1; Length 302;
Best Local Similarity 94.7%; Pred. No. 3.2e-94;
Matches 286; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
Qy 78 GNINLGSANPAOPTDFLKVIGKNGYKVLAKRSGAGFAVAVKVLQKKSILKKKEQ 137
Db 1 GNINLGSANPAOPTDFLKVIGKNGYKVLAKRSGAGFAVAVKVLQKKSILKKKEQ 60
Qy 138 SHIAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDVYNGGELFFHLQREHRELEPRAR 197
Db 61 SHIAERNVLLKNVRHPFLVGLRYSFOTPEKLYFVLDVYNGGELFFHLQREHRELEPRAR 120
Qy 198 FYAAEVASAIYLHSLNIIYRDLKPNILLDCQGHVVLTFGLCKEGVEPEDTSTFCGT 257
Db 121 FYTAEVASAIGYLSHSLNIIYRDLKPNILLDCQGHVVLTFGLCKEGVEPEDTSTFCGT 180
Qy 258 PEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVDSQMYENILHQPQLQIPGGR 317
Db 181 PEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVDSQMYENILHQPQLQIPGGR 240
Qy 318 TVAACDLLOSLHKKQRLGSKADFLKLEIKHNVFFSPINWDDLYHKRLTTPFPNPNVTGPA 377
Db 241 TVAACDLLOSLHKKQRLGSKADFLKLEIKHNVFFSPINWDDLYHKRLTTPFPNPNVTGPA 300
Qy 378 DL 379
Db 301 DL 302
RESULT 9
Q5H8Y4_HUMAN
ID Q5H8Y4_HUMAN PRELIMINARY; PRT; 285 AA.
AC Q5H8Y4
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE OTTHUMP0000031704.
GN Name=SGK2; ORFNames=RPI-138B7.2-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; Z98752; CAI42314.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 285 AA; 32130 MW; A3493A701ABB4542 CRC64;
Query Match 64.8%; Score 1497; DB 2; Length 285;
Best Local Similarity 99.6%; Pred. No. 2.1e-91;
Matches 283; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 61 MNSGPAGTSPQPSRANGNINLGSANPNAPQPTDFLKVIGKNGYKVLAKRSGAGFA 120
Db 1 MNSGPAGTSPQPSRANGNINLGSANPNAPQPTDFLKVIGKNGYKVLAKRSGAGFA 60
Qy 121 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDVYNGGE 180
Db 61 YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFOTPEKLYFVLDVYNGGE 120
Qy 181 LFPHLOQRERFLPRARFYAAEVASAIYLHSLNIIYRDLKPNILLDCQGHVVLTFGL 240
Db 121 LFPHLOQRERFLPRARFYAAEVASAIYLHSLNIIYRDLKPNILLDCQGHVVLTFGL 180
Qy 241 CKGVPEPDITSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVDS 300
Db 181 CKGVPEPDITSTFCGTPEYLAPEVLRKEPYDRAVDMWCLGAVLYEMLHGLPPFYSDVDS 240
Qy 301 QMYENILHQPQLQIPGGRITVAACDLLOSLHKKQRLGSKADFL 344
Db 241 QMYENILHQPQLQIPGGRITVAACDLLOSLHKKQRLGSKADFL 284
RESULT 10
Q4S7Y9_TETNG
ID Q4S7Y9_TETNG PRELIMINARY; PRT; 350 AA.
AC Q4S7Y9
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 9 SCAF14710, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0022577001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cottolico L., Poulain J., De Berardinis V.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet P., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of

CC MPF (By similarity).
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: CAAE01014710; CAG03243.1; -; Genomic_DNA.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_A; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TyrK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 350 AA; 39571 MW; 56BF9C5C2889D924 CRC64;

Query Match 62.8%; Score 1450.5; DB 2; Length 350;
Best Local Similarity 77.1%; Pred. No. 3.3e-88;
Matches 270; Conservative 36; Mismatches 43; Indels 1; Gaps 1;
QY 76 ANGINLSPSNAQPTDFDLKVGKNGYKVLAKRSDGAFYAVKVLQKKILKKK 135
DB 2 SHDDVNLSPSANPHARTDFDLFLAVIGKTFGKVLAKKHTDSFVAVKVLQKKILKKK 61
QY 136 EQSHMAERSVLLKNVRHPELVGLRYSFQPEKLYFVLDVYNGGELFFHLQRRRRFLEPR 195
DB 62 EQKNMAERNVLLKSLKHPFLVRLHYSFQAEKLYFVLDVYNGGELFFHLQRRRCFSEPR 121
QY 196 ARFYAAEVAASAIQYLHSLNIYDLPENILLDCQGHVLTDFGLCKEGVEPDTTSTFC 255
DB 122 ARFYAAEVAASAIQYLHSLNIYVLDLPENILLDSQGHVLTDFGLCKEGVEPDTTSTFC 181
QY 256 GTEPEYLAPEVLRKEPYDRAVDWVCLGAVLYEMHLGLPPFYSDQVSMYENILHQPILQIPG 315
DB 182 GTEPEYLAPEVLRKEPYDRTVWVCLGAVLYEMISLPPFYSDVGVWYDGLHKPLQLPP 241
QY 316 GRTVAACDLQSLHKKQORQLSGKADFLKHNHVFSPINWDDLYHKRLTTPFPNPNVTG 375
DB 242 GKSDAVCSLLVGLLQKHQRLGALADFLKHNHVFPTPINWDDLYHKRLTTPFPNPNVVG 301
QY 376 PADLKHPDPEFTQEAIVSKSIGCTPDTVASSSGASSAFGLGSYAPEDDDIL 425
DB 302 PADTQHIDPEFTREVMVSSVSQTPEFTASAS-ASNAPNGFSFVATEDSFL 350

RESULT 11
Q5Q0U5_FUNHE PRELIMINARY; PRT; 431 AA.
AC Q5Q0U5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serum and glucocorticoid-regulated kinase.
GN Names=SGK;
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Sato J.D., Clarke C.C., Stanton B.A.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY800243; AAV80429.1; -; mRNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_A; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TyrK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 431 AA; 48870 MW; 91C80821F64B454D CRC64;
Query Match 62.5%; Score 1445.5; DB 2; Length 431;
Best Local Similarity 69.6%; Pred. No. 9.2e-88;
Matches 270; Conservative 51; Mismatches 56; Indels 11; Gaps 4;
QY 41 PTLSCLLPVPPELPHDHCYRMNSPAGTSPQSPRANGNINLGPSANPNAQPTDFDLKV 100
DB 52 PEVQSILNLTTPQDPE--LMNSNP--SPPPSPSQ--QINLGPSNPSAKPSDFHLKV 103
QY 101 IGKNGYKVLAKRSDGAFYAVKVLQKKILKKQSHIMAERSVLLKNVRHPELVGLR 160
DB 104 IGKSGFGKVLARHRTDDQFYAVKVLQKAIKKKEKHIMSERNVLLKNVRHPELVGLH 163
QY 161 YSFQPEKLYFVLDVYNGGELFFHLQRRRRFLEPRARFYAAEVAASAIQYLHSLNIYRDL 220
DB 164 YSFQADKLYFVLDVYNGGELFFHLQRRRCFLEPRARFYSAEIASALGSLHSLNIYRDL 223
QY 221 KPENILLDCQGHVLTDFGLCKEGVEPDTTSTFCGTEPEYLAPEVLRKEPYDRAVDWVCL 280
DB 224 KPENILLDSQGHVLTDFGLCKENIEPNTGTTSTFCGTEPEYLAPEVLRKEPYDRTVWVCL 283
QY 281 GAVLYEMHLGLPPFYSDQVSMYENILHQPILQIPGRTVAACDLQSLHKKQORQLSGK 340
DB 284 GAVLYEMLYGLPPFYSDVSRNTAEYDNLNKLQKPNISYARHLLEGLLQKDKTKRLGCK 343
QY 341 ADPLETEKNHVFSPINWDDLYHKRLTTPFPNPNVTGPDALKHPDPEFTQEAIVSKSIGCTPD 400
DB 344 DDFTEIKHNHVFSPINWDDLNKAKMTTPFPNPNVTGENDLRHFDPEFTDPEVPSSIGCSPD 403
QY 401 ---TVASSSGASSAFGLGSYAPEDDDIL 425
DB 404 CALATASIKEAAEAFVGSYAFSPMSYLL 431

RESULT 12
Q72TW4_BRARE PRELIMINARY; PRT; 433 AA.
AC Q72TW4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serum/glucocorticoid regulated kinase.
GN Names=sgk;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney, and Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences,"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 (2)
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 RG NIH MGC Project;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RG NIH MGC Project;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and
 monomeric catalytic subunit). Translocates into the nucleus
 (monomeric catalytic subunit) (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC052134; AAH52134.1; -; mRNA.
 DR EMBL; BC067618; AAH67618.1; -; mRNA.
 DR HSSP; P31751; 1WRV.
 DR Ensembl; ENSDARG000025522; Danio rerio.
 DR ZFIN; ZDB-GENE-030131-2860; sgk.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase; CAMP.
 SQ SEQUENCE 433 AA; 49983 MW; FZAA4771E245FF56 CRC64;

Query Match 62.3%; Score 1440.5; DB 2; Length 433;
 Best Local Similarity 69.8%; Pred. No. 2e-87;
 Matches 271; Conservative 49; Mismatches 57; Indels 11; Gaps 4;

QY 41 PTUSCLLLVPPELPHDCHYRMNSSPAGTSPQPSRANGNINLGSANPNAPQTFDFLKV 100
 Db 54 PEVQSILNLTTPQ---DVELMNGNP---SPPPSPSQ---QINLGPSSNPTAKPSDFDFLKV 105
 QY 101 IKGNYGKGVLLAKRSDGAFYAVKVLQKSKILKKKQSHIMARSVLLKNVRPFLVGLR 160
 Db 106 IKGSGFGKVLARHRSDKGFYAVKVLQKSKILKKKQSHIMARSVLLKNVRPFLVGLR 165
 QY 161 YSFQTPKLVFLVDYVNGGELFFHLQRRERFLPRARFYAAEVAASATGLHSLNIIYRL 220

Db 166 YSFQTTDKLVFLVDYVNGGELFFHLQRRERFLPRARFYAAEVAASATGLHSLNIIYRL 225
 QY 221 KPNILLDCOGHVLTDFGLCKEGVPEPDTSTFCGTPYLAPEVLKPEPVDRAVDWCL 280
 Db 226 KPNILLDSQGHILDTDFGLCKENIEPNTTSTFCGTPYLAPEVLKPEPVDRTVDWCL 285
 QY 281 GAVLYEMLHGLPPFYSDQVSQMYENILHQLPQIPGGRTVAACDILQLLHKDQORLGSK 340
 Db 286 GAVLYEMLYGLPPFYSRNTAEYMDNLTLPQLKPNISNAARHLEGLQKDRKRLGPT 345
 QY 341 ADFLKIKNVFFSPINWDDLYHRLTPFPNPNTGPAADLKHPDPEFTQEAHSVSGICTPD 400
 Db 346 DDFTEIKNHFSPINWDDLNAAKLTTPFPNPNTGPNDLRHFDPPEFTDEPVPNSIGGSPD 405
 QY 401 T---VASSSGASSAFLGFSYAPEDDDIL 425
 Db 406 SALVTSSITEATFAFLGFSYAPAMD SYL 433

RESULT 13

Q6UI19_CHICK

ID Q6UI19_CHICK PRELIMINARY; PRT; 432 AA.

AC Q6UI19;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Serum-and glucocorticoid-induced kinase.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Malkiewicz S.A., Porter T.E.;

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AV380825; AAQ88435.1; -; mRNA.

DR HSSP; P05132; 1ATP.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000961; Pkinase C.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR008271; Ser_thr_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR Pfam; PF00433; Pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00133; S_TK_X; 1.

DR SMART; SM00220; S_TK; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

KW Kinase.

SQ SEQUENCE 432 AA; 48890 MW; 83AB52AFF2609953 CRC64;

Query Match 61.7%; Score 1427; DB 2; Length 432;

Best Local Similarity 68.3%; Pred. No. 1.6e-86;

Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 38 PPTPTLSCLLVPPELPHDCHYRMNSSPAGTSPQPSRANGNINLGSANPNAPQTFDF 97
 Db 53 PEVQSILKISQPEL-----MNA NP--SPPPSPSQ---QINLGPSSNPHAKPSDFH 101
 QY 98 LKVIKGNVGVLLAKRSDGAFYAVKVLQKSKILKKKQSHIMARSVLLKNVRPFLV 157
 Db 102 LKVIKGNVGVLLAKRSDGAFYAVKVLQKSKILKKKQSHIMARSVLLKNVRPFLV 161
 QY 158 GLRYSFQTPKLVFLVDYVNGGELFFHLQRRERFLPRARFYAAEVAASATGLHSLNIIY 217

Db 162 GLHFSQTADKLVFLVDYINGGELFYHLQRCRCFLPRARFYAAETASALGYLHSLNIVY 221
 QY 218 RDLKPNENILDCQGHVVLTDFGLCKGVEPEDTTSTFCGTPEYLAPEVLKPEYDRADVW 277
 Db 222 RDLKPNENILDCQGHVVLTDFGLCKENIEHNGTTSTFCGTPEYLAPEVLKQPYDRVDW 281
 QY 278 WCLGAVLYEMLHGLPPYSODVSMYENILHQPLOIPGGRTVAAACDLQSLHKKQORL 337
 Db 282 WCLGAVLYEMLHGLPPYSRNTAEYDNLKPLQKPNITNSARNLEGLLQKORTKRL 341
 QY 338 GSKADFLKINHVFFSPINWDDLYHKRLTPPFPNVTGPADLKHDFPEFTQEAVSIGC 397
 Db 342 GAKEDFTKINHVFFSPINWDDLYHKRLTPPFPNVTGPADLKHDFPEFTQEAVSIGC 401
 QY 398 TPDVT---ASSGASSAFGLGSYAPEDDDIL 425
 Db 402 SPDSILITASVKEAAEAFGLGSYAPVDSPL 432
 RESULT 14
 O93524 XENLA PRELIMINARY; PRT; 434 AA.
 ID AC O93524;
 DT 01-NOV-1998 (T-EMBLrel. 08, Created)
 DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Renal tubule;
 RX MEDLINE=99162637; PubMed=10051674; DOI=10.1073/pnas.96.5.2514;
 RA Chen S.-Y., Bhargava A., Mastroberardino L., Meijer O.C., Wang J.,
 Buse P., Firestone G.L., Verrey F., Pearce D.;
 RT "Epithelial sodium channel regulated by aldosterone-induced protein
 sgk.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2514-2519(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Renal tubule;
 RA Chen S.-Y., Pearce D.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and
 monomeric catalytic subunit). Translocates into the nucleus
 (monomeric catalytic subunit) (By similarity).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF057138; AAC62398.1; -; mRNA.
 DR HSP; P31751; 1MRV.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; I.
 DR Pfam; PF00433; Pkinase C; 1.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00133; S TK X; 1.
 DR SMART; SM00220; S TKG; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Cell cycle; Cell division; Hypothetical protein; Kinase;
 KW Nuclear protein; Nucleotide-binding; Serine/threonine-protein kinase;
 KW Transferase; camp.
 SQ SEQUENCE 434 AA; 49130 MW; 4A061E3B86AA6F61 CRC64;

Query Match 61.7%; Score 1425.5; DB 2; Length 434;
 Best Local Similarity 69.0%; Pred. No. 28-86;
 Matches 261; Conservative 59; Mismatches 47; Indels 11; Gaps 3;
 QY 51 PPELDHCYRMNSSPAGTPSPQPSRANGINILGPSANPNNAQPTDFDLKVIKGNVGVYL 110
 Db 65 PPQEP-LLNENSSPPSPSQ-----INLGPSSNPHAKPSDFQFLAIKGSFGKVL 116
 QY 111 LAKRSDDGAFYAVKVLQKSLKKEQSHIMAEVSLLKNVRHPLVGLRYSFQTEPKLY 170
 Db 117 LARHOSDEKFAVKVLQKAILKKEEKHIMSERVLLKNVKHPLVGLHFSFQTTSLRY 176
 QY 171 FVLVDYNGGELFHLQRRERFLEPRARFYAAVSAIGAIVLHSLNIIYRLDKPENILLDCQ 230
 Db 177 FLDYINGGELFYHLQRCRCFLPRARFYAAETASALGYLHSLNIIYRLDKPENILLDCQ 236
 QY 231 GHVLTDFGLCKGVEPEDTTSTFCGTPEYLAPEVLKPEYDRADVWMLCGAVLYEMLHG 290
 Db 237 GHVLTDFGLCKENIEPNTTSTFCGTPEYLAPEVLKQPYDRTVDMWMLCGAVLYEMLYG 296
 QY 291 LPFFYSQDVSMYENILHQPLOIPGGRTVAAACDLQSLHKKQORLQSKADFLKINHV 350
 Db 297 LPFFYSRNTAEYDNLKPLQKPNITNSARNLEGLLQKORTKRIKANDFMEIKNHI 356
 QY 351 FSPINWDDLYHKRLTPPFPNVTGPADLKHDFPEFTQEAVSIGCTPTDV---ASSSG 407
 Db 357 FSPINWDDLYHKRLTPPFPNVTGPADLKHDFPEFTQEAVSIGCTPTDV---ASSSG 416
 QY 408 ASSAFGLGSYAPEDDDIL 425
 Db 417 AAETAFGLGSYAPVDSPL 434
 RESULT 15
 SGK1 RABIT STANDARD; PRT; 431 AA.
 ID AC O9XTI8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Serine/threonine-protein kinase Sgk1 (EC 2.7.1.37)
 DE (Serum/glucocorticoid-regulated kinase 1).
 GN Name=SGK; Synonym=SGK1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=New Zealand white;
 RX MEDLINE=99287894; PubMed=10358046; DOI=10.1074/jbc.274.24.16973;
 RA Naray-Fejes-Toth A., Canessa C., Cleaveland E.S., Aldrich G.,
 RA Fejes-Toth G.;
 RT "sgk is an aldosterone-induced kinase in the renal collecting duct.
 Effects on epithelial Na+ channels.";
 RL J. Biol. Chem. 274:16973-16978(1999).
 CC -!- FUNCTION: Protein kinase that plays an important role in
 activating certain potassium, sodium, and chloride channels,
 suggesting an involvement in the regulation of processes such as
 cell survival, neuronal excitability, and renal sodium excretion.
 CC May be a key component of cellular stress response. Phosphorylates
 CC NEDD4L, which leads to its inactivation and to the subsequent
 CC activation of various channels and transporters such as ENAC,
 CC Kv1.3, or EAAT1 (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Interacts with NEDD4 and NEDD4L (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear, upon
 phosphorylation (By similarity).
 CC -!- PTM: Regulated by phosphorylation. Phosphoinositide 3-kinase (PI3-
 kinase) pathway promotes phosphorylation at Ser-422 which in turn
 increases the phosphorylation of Thr-256 by PDPK1 (By similarity).
 CC -!- PTM: Ubiquitinated by NEDD4L; which promotes proteasomal

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CC      degradation (By similarity).
CC      -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AF139633; AAD43303.1; -; mRNA.
CC      HSP; P31751; 1GZK.
CC      InterPro; IPR000961; Pkinase_C.
CC      InterPro; IPR000719; Prot_kinase.
CC      InterPro; IPR008271; Ser_thr_pkin_AS.
CC      InterPro; IPR002290; Ser_thr_pkinase.
CC      Pfam; PF00069; Pkinase; 1.
CC      Pfam; PF00433; Pkinase_C; 1.
CC      ProDom; PD000001; Prot_kinase; 1.
CC      SMART; SM00133; S_TK_X; 1.
CC      SMART; SM00220; S_TKC; 1.
CC      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC      PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC      Apoptosis; ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
CC      Phosphorylation; Serine/threonine-protein kinase; Transferase;
CC      Ub1 conjugation.
CC      DOMAIN 98      Protein kinase.
CC      NP_BIND 104 112  ATP (By similarity).
CC      MOTIF 131 141  Nuclear localization signal (By
CC      similarity).
CC      ACT_SITE 222 222  Proton acceptor (By similarity).
CC      BINDING 127 127  ATP (By similarity).
CC      MOD_RES 256 256  Phosphothreonine (by PDPK1) (By
CC      similarity).
CC      MOD_RES 422 422  Phosphoserine (By similarity).
CC      SEQUENCE 431 AA; 48999 MW; 354898A77E8E38FD CRC64;

Query Match      61.6%; Score 1423; DB 1; Length 431;
Best Local Similarity 70.0%; Pred. No. 2.9e-86;
Matches 266; Conservative 55; Mismatches 45; Indels 14; Gaps 4;

QY 49 PVPPELDPHCVRMNSSPAGTSPQPSRANGNINLPSANPNAQPTDFDLKVGKNGYK 108
DB 63 PQPEL-----NNANP--SPPSPSQ---QINLGPSSNPFAKPSDFHLKVIKGSFGK 111
QY 109 VLLAKRSDGAFYAVKVLQKSLKKKEQSHMAERSVLLKNVHPHVLGLRYSPQTPK 168
DB 112 VLLARHKAEEAFYAVKVLQKSKAILKKKEKHIMSERVLLKNVHPHVLGLHFSFQADK 171
QY 169 LYFVLDYVNGELFFHLQRRERFLEPRFVAEVAASAGLYHLSLNIYRDLKPENILLD 228
DB 172 LYFVLDYVNGELFYHLQRECFLEPRFVAEIASALGYHLSLNIYRDLKPENILLD 231
QY 229 CQGHVLTDFGLCKGEVEEDTSTFCGTPYLAPEVLRKEPYDRAVDMWCLGAVLYEML 288
DB 232 SQGHVLTDFGLCKENIEHNGTTSTFCGTPYLAPEVLRKEPYDRTVDMWCLGAVLYEML 291
QY 289 HGLPPFYSDVQWYENILHQLQIPGGRITVAACDLLOSLHLHKDQORGLSKADFLKIN 348
DB 292 YGLPPFYSRNTEMYDNLNKLQLENITNSARHLLGLELLQKDRTKRLGAKDDFMEIRN 351
QY 349 HVFFSPINDDLYHKRLTPFPNPNVTGPADLKHFDPDFTQEAVSKSIGCTPDTV---ASS 405
DB 352 HVFFSLINDDLLNKKITFPFPNPNVSGPSDLRHFDDEFTPEVPSSIGRSPDSILITASV 411
QY 406 SGASSAFLGFSYAPEDDDIL 425
DB 412 KEAAEAPLGFSYAPPMDSFL 431
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